

score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

OM nucleic - nucleic search, using sw model

(without alignments)  
15094.505 Million cell updates/sec

Title: US-09-966-881-13

Sequence: 1 TGTTCCTCCTTCGATCACA.....TCCCCTCTCCTATGGATNG 806

Scoring table: IDENTITY\_NUC

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

1:	gb_ba:	*
2:	gb_hng:	*
3:	gb_in:	*
4:	gb_om:	*
5:	gb_ov:	*
6:	gb_pat:	*
7:	gb_ph:	*
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12:	gb_sy:	*
13:	gb_un:	*
14:	gb_vl:	*
15:	em_ba:	*
16:	em_fun:	*
17:	em_hum:	*
18:	em_in:	*
19:	em_mu:	*
20:	em_om:	*
21:	em_ov:	*
22:	em_or:	*
23:	em_pat:	*
24:	em_ph:	*
25:	em_pl:	*
26:	em_ro:	*
27:	em_sts:	*
28:	em_un:	*
29:	em_vl:	*
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32:	em_hng_other:	*
33:	em_hng_mus:	*
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39:	em_hngo_hum:	*
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41:	em_hngo_other:	*

Pred. No. is the number of results predicted by chance to have a

Result		Query			DB		ID	Description
No	Score	Match	length					
1	778	96.5	806	6	A70152	A70152	Sequence	13
2	612.4	76.0	1788	8	AF206320	AF206320	Musa acum	18
3	591.8	73.4	748	6	AB3011	AB3011	Sequence	11
4	591.2	73.3	745	6	AB3004	AB3004	Sequence	11
5	588.8	73.1	793	6	MA29991	MA29991	Sequence	8
6	588.8	73.1	793	6	MA299965	MA299965	Musa acum	11
7	572.2	71.0	727	6	AB3014	AB3014	Sequence	21
8	543.8	67.5	727	6	A70155	A70155	Sequence	16
9	536	66.5	724	6	A70157	A70157	Sequence	18
10	510.8	63.4	704	6	AB3002	AB3002	Sequence	7
11	496.8	61.6	706	6	AB3010	AB3010	Sequence	19
12	174.4	21.6	127202	2	OSJN0022	OSJN0022	Oryza sat	19
13	169.4	21.0	1633	8	AY085026	AY085026	Arabidops	6
14	152	18.9	90142	8	ATAC016827	ATAC016827	Arabidops	10
15	151	18.7	823	6	AB3003	AB3003	Sequence	10
16	150	18.6	1408	8	FX063550	FX063550	Fraxia x	10
17	148	18.4	1523	8	AY086099	AY086099	Arabidops	10
18	144.8	18.0	1496	8	AF206319	AF206319	Musa acum	14
19	144.4	17.9	749	6	AB2999	AB2999	Sequence	6
20	143.2	17.8	1462	8	MAPEL	MAPEL	Sequence	6
21	142.8	17.7	842	6	A70156	A70156	Sequence	17
22	141.4	17.5	708	6	AB3002	AB3002	Sequence	17
23	141	17.5	1525	8	AY050404	AY050404	Arabidops	9
24	141	17.5	1556	8	AY050795	AY050795	Arabidops	12
25	134.6	16.7	687	6	A70153	A70153	Sequence	14
26	134.6	16.7	687	8	MA299977	MA299977	Musa acum	14
27	133.2	16.5	5368	8	AF339024	AF339024	Fraxia	17
28	131.6	16.3	772	6	AB3010	AB3010	Sequence	17
29	131.6	16.3	772	8	MA299970	MA299970	Musa acum	12
30	131	16.3	758	6	AB3005	AB3005	Sequence	12
31	130.4	16.2	1431	8	AY058197	AY058197	Arabidops	13
32	129.2	16.0	794	6	AB3006	AB3006	Sequence	20
33	128.8	16.0	728	6	AB3013	AB3013	Sequence	15
34	128.4	15.9	745	6	AB3008	AB3008	Sequence	15
35	127.2	15.8	1782	8	AY087724	AY087724	Arabidops	15
36	127	15.8	1065	8	AY066033	AY066033	Arabidops	16
37	127	15.8	1459	8	AY065034	AY065034	Arabidops	16
38	127	15.8	1788	8	AY054200	AY054200	Arabidops	16
39	126.2	15.7	731	6	AB3009	AB3009	Sequence	16
40	124	15.4	1440	6	AX005936	AX005936	Sequence	16
41	124	15.4	1440	8	ZEPCLY	ZEPCLY	Sequence	16
42	123.6	15.3	4143	8	AF339025	AF339025	Fraxia	16
43	122.6	15.2	100079	8	TI611	TI611	Sequence	16
44	122	15.1	61712	8	AB017061	AB017061	Arabidops	16
45	122	15.1	81652	8	AB008265	AB008265	Arabidops	16

## ALIGNMENTS

LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL
A70152	Sequence 13 from Patent WO9811228.	A70152	A70152.1	GI:4774567	unidentified.	unidentified	unclassified.	1 (Bases 1 to 806)	Seymour G.B., Bird,C.R. and Medina-Suarez,R.D.	GENETIC CONTROL OF FRUIT RIPENING
									Patent: WO 9811228-A 13 19-MAR-1998;	SEYMOUR GRAHAM BARRON (GB)

FEATURES  
source  
Location/Qualifiers  
1. 806  
/organism="unidentified"  
/db\_xref="taxon:32644"  
/clone="U-068"

BASE COUNT 157 a 229 c 212 g 180 t 28 others

Query Match 96.5%; Score 778; DB 6; Length 806;  
Best Local Similarity 100.0%; Pred. No. 3.8e-193;  
Matches 806; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTTCCTCTCGATGACATCTTTTGTCTCTGGAAACGTGAGAGTGAGAGGCG 60  
DB 1 TGTTCCTCTCGATGACATCTTTTGTCTCTGGAAACGTGAGAGTGAGAGGCG 60  
QY 61 GCATGACGGGGGTTAAGATGATTCCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120  
DB 61 GCATGACGGGGGTTAAGATGATTCCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120  
QY 121 CTGGTTTGAACGAGGCTCGGGGGTGGATTGGAAGAGAGTCTCTGCTCGAGGAAT 180  
DB 121 CTGGTTTGAACGAGGCTCGGGGGTGGATTGGAAGAGAGTCTCTGCTCGAGGAAT 180  
QY 181 GCGGAGCATCGCGGAGGAGCTTGAGAGAGCTCCGCGAAGCGGACCGCGATGCT 240  
DB 181 GCGGAGCATCGCGGAGGAGCTTGAGAGAGCTCCGCGAAGCGGACCGCGATGCT 240  
QY 241 TCCTTGAAGAGGGCTGTAAACCCGGGAGAGAGCCGAGTCAGAGACCCGAGAG 300  
DB 241 TCCTTGAAGAGGGCTGTAAACCCGGGAGAGAGCCGAGTCAGAGACCCGAGAG 300  
QY 301 GTTGCTTCGAGGCTCTGATGACATATATCAACAGCAGGCTCGACATCTCTGTTAT 360  
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QY 361 CTGCTGCGGCTTGAGCAACCCGATGAGAGCTGCGGGGTGCGACCTGATGGCAT 420  
DB 361 CTGCTGCGGCTTGAGCAACCCGATGAGAGCTGCGGGGTGCGACCTGATGGCAT 420  
QY 421 GTCAACGAAAAAGCTCGCTGACTGCGGATGGCTTTGGAGCAGCAGNATANGGCG 480  
DB 421 GTCAACGAAAAAGCTCGCTGACTGCGGATGGCTTTGGAGCAGCAGNATANGGCG 480  
QY 481 CCGGAGCGGGAATTTGTTCTGTTGACAGACTCGGGGAGCAGNATANGTCCGTC 540  
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QY 541 GCGCGGAGACATTAAATACCCGCTCTCCAGAAAGTTGCCCTCTGGGATCCCTTT 600  
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DB 661 CGATGAGCNCNGTCTCTCTGATGCAATGGCAATGGCCCTGCTGACCAACCAATTTCN 720  
QY 721 TCCCAACACNTCTTCTCANTNGCTCNCNCCCAATGCAACCCCGGAATTTCTNGT 780  
DB 721 TCCCAACACNTCTTCTCANTNGCTCNCNCCCAATGCAACCCCGGAATTTCTNGT 780  
QY 781 CCCCNCCTCCCTCTCTCTATGATNG 806  
DB 781 CCCCNCCTCCCTCTCTCTATGATNG 806

RESULT 2  
AF206320 1788 bp mRNA linear PLN 21-DEC-1999  
LOCUS AF206320  
DEFINITION Musa acuminata pectate lyase 2 (PL2) mRNA, complete cds.

ACCESSION AF206320  
VERSION AF206320.1 GI:6606533  
KEYWORDS  
SOURCE Musa acuminata  
ORGANISM Musa acuminata  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Zingiberales; Musaceae; Musa.

REFERENCE 1 (bases 1 to 1788)  
Ong,C.K., Pua,E.C. and Liu,P.  
TITLE Molecular cloning and characterization of pectate lyase in banana  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 1788)  
Ong,C.K., Pua,E.C. and Liu,P.  
TITLE Direct Submission  
JOURNAL Submitted (18-NOV-1999) Department of Biological Sciences, National University of Singapore, 10 Kent Ridge Crescent, Singapore 119260

FEATURES  
source  
Location/Qualifiers  
1. 1788  
/organism="Musa acuminata"  
/cultivar="Williams"  
/db\_xref="taxon:4641"  
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78. 1442  
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/translation="MTAGLRWIPPLLLLLGLFLLVNGSRWIGTSRSGSRNGASR  
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GLTRVAYIDVPLMIFPKHDMETLKEELNFKETIDGAVNVHILANGACITIOYT  
NVIIGHIHDCKPTGAMAYRSSPSHGMETMDGDAVSIFFSSHIWVHDSISLND  
GLVDYAVGSTATITVSNNYFTHHNEVHLGHTDSYARSDINQVITAEHREGLIORP  
RCHRGFHVNVNDYTHWEMTAIGSAPPTINSQGNRYLAPNPAEVRKRVPTDOST  
WKNMNMRSBGLDLNGLAFPPSGAGASASAYARASFSKAPKPSLVDTLSDAGVLSQV  
GTRC"

BASE COUNT 419 a 473 c 470 g 426 t

Query Match 76.0%; Score 612.4; DB 8; Length 1788;  
Best Local Similarity 88.6%; Pred. No. 1e-149;  
Matches 716; Conservative 0; Mismatches 82; Indels 10; Gaps 6;

QY 1 TGTTCCTCTCGATGACATCTTTTGTCTCTGGAAACGTGAGAGTGAGAGGCG 60  
DB 1 TGTTCCTCTCGATGACATCTTTTGTCTCTGGAAACGTGAGAGTGAGAGGCG 60  
QY 15 TGTTCCTCTCGATGACATCTTTTGTCTCTGGAAACGTGAGAGTGAGAGGCG 74  
DB 15 TGTTCCTCTCGATGACATCTTTTGTCTCTGGAAACGTGAGAGTGAGAGGCG 74  
QY 61 GCATGACGGCGGGTTAAGATGATTCCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120  
DB 61 GCATGACGGCGGGTTAAGATGATTCCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120  
QY 121 CTGGTTTGAACGAGGCTCGGGGGTGGATTGGAAGCAGAGTCTCTGCTGAGGAAT 180  
DB 121 CTGGTTTGAACGAGGCTCGGGGGTGGATTGGAAGCAGAGTCTCTGCTGAGGAAT 180  
QY 135 CTGGTTTGAACGAGGCTCGGGGGTGGATTGGAAGCAGAGTCTCTGCTGAGGAAT 194  
DB 135 CTGGTTTGAACGAGGCTCGGGGGTGGATTGGAAGCAGAGTCTCTGCTGAGGAAT 194  
QY 181 GCGGAGCATCGGGGAGGAGCTTGAGAGAGGCTCCGCGAAGCGAGCAGCGCGATGCT 240  
DB 181 GCGGAGCATCGGGGAGGAGCTTGAGAGAGGCTCCGCGAAGCGAGCAGCGCGATGCT 240  
QY 195 GCGGAGCATCGGGGAGGAGCTTGAGAGAGGCTCCGCGAAGCGAGCAGCGCGATGCT 254  
DB 195 GCGGAGCATCGGGGAGGAGCTTGAGAGAGGCTCCGCGAAGCGAGCAGCGCGATGCT 254  
QY 241 TCCTTGAAGAGAGGCTGTAAACCCGAGCAGAAACCCAGTGCAGCAGCCCGAGAGAG 300  
DB 241 TCCTTGAAGAGAGGCTGTAAACCCGAGCAGAAACCCAGTGCAGCAGCCCGAGAGAG 300  
QY 255 TCCTTGAAGAGAGGCTGTAAACCCGAGCAGAAACCCAGTGCAGCAGCCCGAGAGAG 314  
DB 255 TCCTTGAAGAGAGGCTGTAAACCCGAGCAGAAACCCAGTGCAGCAGCCCGAGAGAG 314  
QY 301 GTTGCTTCGAGGCTCTGATGACATATATCAACAGCAGGCTCGACATCTTGGTTAT 360  
DB 301 GTTGCTTCGAGGCTCTGATGACATATATCAACAGCAGGCTCGACATCTTGGTTAT 360  
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DB 315 GTTGCTTCGAGGCTCTGATGACATATATCAACAGCAGGCTCGACATCTTGGTTAT 374  
QY 361 CTGCTGCGGCTTGAGCAACCCGATGAGAGCTGCGGGGTGCGACCTGATGGCAT 420  
DB 361 CTGCTGCGGCTTGAGCAACCCGATGAGAGCTGCGGGGTGCGACCTGATGGCAT 420

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OY 421 GTCAACAGAAAAAGCTGCTGACTGCGGCAATGAGCTTTGGACGCAACGNAATANGTGC 480
DB 435 GTCAACAGAAAAAGCTGCTGACTGCGGCAATGAGCTTTGGACGCAACGNAATANGTGC 494
OY 481 CGCGAGGAGGAAATTTGTTGCTGTGACAGACTCCGGGACNATGATCCCGGTGAATCTC 540
DB 495 CGCGAGGAGG-AGTTGTACGTTGTGACAGACTCCGGGACNATGAT-CCCGGTGAATCTC 552
OY 541 GCGCGGGAACATTANATACCCCGTCNCCANANGAAGTTGCCCGCTCTGGATCCCTTT 600
DB 553 GCGCGGGAACATTAGATAGAGCGCGCTATCC-AGGACGTGCGCCCTGTGATCCTTT 608
OY 601 AAACNCNANTGGAATCTCNCCTNANGAAGAACTCTTTATGAACAGCTTTAAACNAT 660
DB 609 AAACNCNANTGGAATCTCNCCTNANGAAGAACTCTTTATGAACAGCTTTAAACNAT 667
OY 661 CGATGAGACNCGTGTCTGTCACATTTGCCAATGGCGCTGCTNCCANCCAAATTTTCN 720
DB 668 CGATGAGACNCGTGTCTGTCACATTTGCCAATGGCGCTGCTNCCANCCAAATTTTCN 726
OY 721 TCCCAACNTCTTCTTCNTNGCCTCCNC--TCCCAATGCAACCCCGGGAATTCCTN 778
DB 727 TCACCAACGTCATCATCCACGCGCTCCACATCCACGACTGCAAGCCGGAATTCGCA 786
OY 779 GTCCCNCTCCCTCTCTCTATGATNG 806
DB 787 TGTGCGCACTCTCTCTCTCTATGATNG 814

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## RESULT 3

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LOCUS A83011 748 bp DNA linear PAT 21-JAN-2000
DEFINITION Sequence 18 from Patent WO9853085.
ACCESSION A83011
VERSION A83011.1 GI:6732491
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 748)
AUTHORS Seymour,G.B. and Bird,C.R.
TITLE GENETIC CONTROL OF FRUIT RIPENING
JOURNAL Patent: WO 9853085-A 18 26-NOV-1998;
SEYMOUR GRAHAM BARRON (GB); ZENECA LTD (GB)
FEATURES
SOURCE location/Qualifiers
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/db_xref="taxon:32644"
/clone="U-113"

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BASE COUNT 154 a 211 c 206 g 163 t 14 others
ORIGIN
Query Match 73.4%; Score 591.8; DB 6; Length 748;
Best Local Similarity 91.7%; Pred. No. 2.5e-144;
Matches 664; Conservative 0; Mismatches 52; Indels 8; Gaps 4;

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OY 1 TGTTCCTCTTCATCATCTTTTGTCTGGAACAGTGAGAGGTGACGAGGCG 60
DB 16 TGTTCCTCTTCATCATCTTTTGTCTGGAACAGTGAGAGGTGACGAGGCG 75
OY 61 GCAATGAGGCGGGTTAAGATGATTCCTCTGCTTCTCTCTCTCTCTCTCTCT 120
DB 76 GCAATGAGGCGGGTTAAGATGATTCCTCTGCTTCTCTCTCTCTCTCTCTCT 135
OY 121 CTGTTTTGAACGAGGTGCGGGGTGATTTGGAACGAGAGTCTCTGCTCGAGAT 180
DB 136 CTGTTTTGAACGAGGTGCGGGGTGATTTGGAACGAGAGTCTCTGCTCGAGAT 195
OY 181 GCGGAGAGTGGCGGAGAGGCTTGAGAGAGGCTTCGGAACGAGAGCGGCGATGCT 240
DB 196 GCGGAGAGTGGCGGAGAGGCTTGAGAGAGGCTTCGGAACGAGAGCGGCGATGCT 255

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OY 241 TCCTTGGAAGAGGCGCTGTAAACCCGGGAGAGAGCGAGTGCAGACCCCGAGAG 300
DB 256 TCCTTGGAAGAGGCGCTGTAAACCCGGGAGAGAGCGAGTGCAGACCCCGAGAG 315
OY 301 GTTGTTCGAGCGCTCTGATGACATTAATCAACAGACGAGGCTCGAGATCTCTGTTAT 360
DB 316 GTTGTTCGAGCGCTCTGATGACATTAATCAACAGACGAGGCTCGAGATCTCTGTTAT 375
OY 361 CTGTGTCGCTGTCAGGCAACCCGATTCGACAGCTCTGCGGTGGACCTGATGGCAT 420
DB 376 CTGTGTCGCTGTCAGGCAACCCGATTCGACAGCTCTGCGGTGGACCTGATGGCAT 435
OY 421 GTCAACAGAAAAAGCTGCTGACTGCGGCAATGAGCTTTGGACGCAACGNAATANGTGC 480
DB 435 GTCAACAGAAAAAGCTGCTGACTGCGGCAATGAGCTTTGGACGCAACGNAATANGTGC 495
OY 481 CGCGAGGAGGAAATTTGTTGCTGTGACAGACTCCGGGACNATGATTCGCGTGAATCTC 540
DB 495 CGCGAGGAGGAAATTTGTTGCTGTGACAGACTCCGGGACNATGATTCGCGTGAATCTC 555
OY 541 GCGCGGGAACATTANATACCCCGTCNCCANANGAAGTTGCCCGCTCTGGATCCCTTT 600
DB 553 GCGCGGGAACATTAGATAGAGCGCGCTATCC-AGGACGTGCGCCCTGTGATCCTTT 608
OY 601 AAACNCNANTGGAATCTCNCCTNANGAAGAACTCTTTATGAACAGCTTTAAACNAT 660
DB 611 AAACNCNANTGGAATCTCNCCTNANGAAGAACTCTTTATGAACAGCTTTAAACNAT 669
OY 661 CGATGAGACNCGTGTCTGTCACATTTGCCAATGGCGCTGCTNCCANCCAAATTTTCN 720
DB 670 CGATGAGACNCGTGTCTGTCACATTTGCCAATGGCGCTGCTNCCANCCAAATTTTCN 727
OY 721 TCCC 724
DB 728 CACC 731

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## RESULT 4

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LOCUS A83004 745 bp DNA linear PAT 21-JAN-2000
DEFINITION Sequence 11 from Patent WO9853085.
ACCESSION A83004
VERSION A83004.1 GI:6732484
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 745)
AUTHORS Seymour,G.B. and Bird,C.R.
TITLE GENETIC CONTROL OF FRUIT RIPENING
JOURNAL Patent: WO 9853085-A 11 26-NOV-1998;
SEYMOUR GRAHAM BARRON (GB); ZENECA LTD (GB)
FEATURES
SOURCE location/Qualifiers
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BASE COUNT 153 a 204 c 203 g 163 t 22 others
ORIGIN
Query Match 73.3%; Score 591.2; DB 6; Length 745;
Best Local Similarity 90.5%; Pred. No. 3.7e-144;
Matches 673; Conservative 0; Mismatches 61; Indels 10; Gaps 5;

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OY 1 TGTTCCTCTTCATCATCTTTTGTCTGGAACAGTGAGAGGTGACGAGGCG 60
DB 7 TGTTCCTCTTCATCATCTTTTGTCTGGAACAGTGAGAGGTGACGAGGCG 66
OY 61 GCAATGAGGCGGGTTAAGATGATTCCTCTGCTTCTCTCTCTCTCTCTCTCT 120
DB 67 GCAATGAGGCGGGTTAAGATGATTCCTCTGCTTCTCTCTCTCTCTCTCTCT 126
OY 121 CTGTTTTGAACGAGGTGCGGGGTGATTTGGAACGAGAGGTCCTCTGCTCGAGAT 180

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Db      127 CTGTTTGAACGAGGTCGGGGGTGATTGGAAGCAGAGAGTCTTGCTCGAGGAAT 186
Oy      181 GGGGAGCATCGCGGAGAGCTTGAGAGAGGCTCCGGAACGCGACAGCGCGATGCT 240
Db      187 GGGGAGCATCGCGGAGAGCTTGAGAGAGGCTCCGGAACGCGACAGCGCGATGCT 246
Oy      241 TCCTTGAAGAGAGGCTGTAAACCGGGGAGCAGAGACCGGAGTGCAGAGCCCGAGAG 300
Db      247 TCCTTGAAGAGAGGCTGTAAACCGGGGAGCAGAGACCGGAGTGCAGAGCCCGAGAG 306
Oy      301 GTTGCTTCGACGGTCTGATGATGACATTAATCAACAGCAGGCTCGCAATCTCTTGTTAT 360
Db      307 GTTGCTTCGACGGTCTGATGATGACATTAATCAACAGCAGGCTCGCAATCTCTTGTTAT 366
Oy      361 CTGCTGTCGGTTTCAGGCAACCGGATGACAGACTGCGGGGTCGAGCCCGATTTGGCAT 420
Db      367 CTGCTGTCGGTTTCAGGCAACCGGATGACAGACTGCGGGGTCGAGCCCGATTTGGCAT 426
Oy      421 GTCACACAG-AAAAAGCTCGCTGACTCGGCAATTTGGCTTGGACGCAACGCMATANGTG 479
Db      427 GTCACACAGAAAAAGCTCGCTGACTCGGCAATTTGGCTTGGACGCAACGCMATANGTG 486
Oy      480 CCGGAGAGGGGAATTTGTTGTTGTGACAGACTCGGGGACNATGATCCCGTGAAATCT 539
Db      487 CCGGAGAGGGG-ANTTGTACGTGTGTGACAGACTCGGGGACNATGAT-CCCGTGAAATCT 544
Oy      540 CCGGAGAGGCACTTANATACCCGTCNTCCANANGAGTTGCCCGCTCTGGGATCCGCT 599
Db      545 CCGGAGAGGCACTTANATACCCGTCNTCCANANGAGTTGCCCGCTCTGGGATCCGCT 600
Oy      600 TAAACNCNANNTGGAATCTCNCNCNANGAAGAACTNTTANGAACAGC--TTTANA 656
Db      601 TAAACNCNANNTGGAATCTCNCNCNANGAAGAACTNTTANGAACAGC--TTTANA 660
Oy      657 CMTGATGACACNCGTCTGCTGTCACATTTGCCATTTGGCGCTGTCNTACCAACCAAT 716
Db      661 ACATCGATGACACNCGTCTGCTGTCACATTTGCCATTTGGCGCTGTCNTACCAAT 720
Oy      717 TTCNTCCCAACNTCTCTTCNT 740
Db      721 TACATCACCAACGTCATCTTCAT 744

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RESULT 5
A83001
LOCUS      A83001      793 bp      DNA      linear      PAT 21-JAN-2000
DEFINITION Sequence 8 from Patent W09853085.
ACCESSION A83001
VERSION    A83001.1 GI:6732481
KEYWORDS
SOURCE     unidentified.
ORGANISM   unidentified.
REFERENCE  1 (bases 1 to 793)
AUTHORS   Seymour,G.B. and Bird,C.R.
TITLE      GENETIC CONTROL OF FRUIT RIPENING
JOURNAL    Patent: WO 9853085-A 8 26-NOV-1998;
SEYMOUR GRAHAM BARON (GB); ZENECA LTD (GB)
FEATURES
Source     1. 793
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BASE COUNT      170 a      222 c      215 g      171 t      15 others
ORIGIN

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Query Match      73.1%; Score 588.8; DB 6; Length 793;
Best Local Similarity 88.7%; Pred. No. 1.6e-143;
Matches 705; Conservative 0; Mismatches 77; Indels 13; Gaps 7;
Oy      1 TGTTCCTCTTCGATCACAATCTTTTGTCTCTGGAAACGTGAGAGTGACGAGGCG 60
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Oy      121 CTGTTTGAACGAGAGTCCGGGGTGTGAAGCAGAGAGTCTTGCTCGAGGAAT 180
Db      128 CTGTTTGAACGAGAGTCCGGGGTGTGAAGCAGAGAGTCTTGCTCGAGGAAT 187
Oy      181 GGGGAGCATCGCGGAGAGCTTGAGAGAGGCTCCCGGAACGCGACAGCGCGATGCT 240
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Db      308 GTTGCTTCGACGGTCTGATGATGACATTAATCAACAGCAGGCTCGCAATCTCTTGTTAT 367
Oy      361 CTGCTGTCGGTTTCAGGCAACCGGATGACAGACTGCGGGGTCGAGCCCGATTTGGCAT 420
Db      368 CTGCTGTCGGTTTCAGGCAACCGGATGACAGACTGCGGGGTCGAGCCCGATTTGGCAT 427
Oy      421 GTCACACAG-AAAAAGCTCGCTGACTCGGCAATTTGGCTTGGACGCAACGCMATANGTG 479
Db      428 GTCACACAGAAAAAGCTCGCTGACTCGGCAATTTGGCTTGGACGCAACGCMATANGTG 487
Oy      480 CCGGAGAGGGGAATTTGTTGTTGTGACAGACTCGGGGACNATGATCCCGTGAAATCT 539
Db      488 CCGGAGAGGGG-ANTTGTACGTGTGTGACAGACTCGGGGACNATGAT-CCCGTGAAATCT 546
Oy      540 CCGGAGAGGCACTTANATACCCGTCNTCCANANGAGTTGCCCGCTCTGGGATCCGCT 599
Db      547 CCGGAGAGGCACTTANATACCCGTCNTCCANANGAGTTGCCCGCTCTGGGATCCGCT 602
Oy      600 TAAACNCNANNTGGAATCTCNCNCNANGAAGAACTNTTANGAACAGC--TTTANA 659
Db      603 TAAACNCNANNTGGAATCTCNCNCNANGAAGAACTNTTANGAACAGC--TTTANA 660
Oy      660 TCGATGACACNCGTCTGCTGTCACATTTGCCATTTGGCGCTGTCNTACCAACCAAT 719
Db      661 TCGATGACACCG-TCGACAGTCCACATTTGCCATTTGGCGCTGTCNTACCAACCAAT 717
Oy      720 NTGCCCAACNTCTCTTCNTCNCNANGAAGAACTNTTANGAACAGC--TTTANA 777
Db      718 ATCACCAACNTCTCTTCNTCNCNANGAAGAACTNTTANGAACAGC--TTTANA 777
Oy      778 NGTCCCGCTCCGCT 792
Db      778 TGTTCCTCTTCGATCACAATCTTTTGTCTCTGGAAACGTGAGAGTGAGACGAGGCG 792

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RESULT 6
MA299965
LOCUS      MA299965      793 bp      mRNA      linear      PLN 03-NOV-1999
DEFINITION Musa acuminata mRNA for putative pectate lyase (type I) (clone pBAN
E022).
ACCESSION MA299965
VERSION    299965
KEYWORDS   299965.1 GI:6249483
SOURCE     Musa acuminata.
ORGANISM   Musa acuminata.
REFERENCE  1 (bases 1 to 793)
AUTHORS   Druy,R., Hortensteiner,S., Donnison,I., Bird,C.R. and Seymour,G.B.
TITLE      Chlorophyll catabolism and gene expression in the peel of ripening
JOURNAL    banana fruits
Physiol. Plantarum 107, 32-38 (1999)

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REFERENCE 2 (bases 1 to 793)  
 AUTHORS Medina-Suarez, R.  
 TITLE Direct Submission  
 JOURNAL Submitted (17-Oct-1997) R. Medina-Suarez, Horticulture Research International, Wellesbourne, Warwick, CV35 9EF, UNITED KINGDOM  
 FEATURES Location/Qualifiers  
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 /cultivar="Grand Nain"  
 /db\_xref="taxon:4641"  
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 ORIGIN  
 Query Match 73.1%; Score 588.8; DB 8; Length 793;  
 Best Local Similarity 88.7%; Pred. No. 1.6e-143;  
 Matches 705; Conservative 0; Mismatches 77; Indels 13; Gaps 7;  
 Oy 1 TGTTCCTCCTTCGATCAGATCTTTTGGCTGCGAAAGCTGAGAGTGAGAGAGGCG 60  
 Db 8 TGTTCCTCCTTCGATCAGATCTTTTGGCTGCGAAAGCTGAGAGTGAGAGAGGCG 67  
 Oy 61 GCAATGACGGGGGTTTAAGATGATTCCTCTGCTTCTTCTTCTGAGGCTTCG 120  
 Db 68 GCAATGACGGGGGTTTAAGATGATTCCTCTGCTTCTTCTTCTGAGGCTTCG 127  
 Oy 121 CTGGTTTGAACGAGAGTGGGGGCTGATTTGAAGAGAGAGAGTCCCTGCTCGAGGAT 180  
 Db 128 CTGGTTTGAACGAGAGTGGGGGCTGATTTGAAGAGAGAGTCCCTGCTCGAGGAT 187  
 Oy 181 GCGGAGCATCGCGGAGGAGCTTGAAGAGAGGCTCCGACGACGACGCGCGATGCT 240  
 Db 188 GCGGAGCATCGCGGAGGAGCTTGAAGAGAGGCTCCGACGACGACGCGCGATGCT 247  
 Oy 241 TCCCTTGAAGAGAGGCTTGAACCCGCGAGCAGAGCCGAGTCAGACGCCCGAGAG 300  
 Db 248 TCCCTTGAAGAGAGGCTTGAACCCGCGAGCAGAGCCGAGTCAGACGCCCGAGAG 307  
 Oy 301 GTTGTTCGACGCTCTGTATGACATTAATCAACAGACGCTCGCATCTCTGTTAT 360  
 Db 308 GTTGTTCGACGCTCTGTATGACATTAATCAACAGACGCTCGCATCTCTGTTAT 367  
 Oy 361 CTGTGTGGGTTGACGCAACCCGATCGACGCTGCTGGCGGTGGACCCCTGATGGCAT 420  
 Db 368 CTGTGTGGGTTGACGCAACCCGATCGACGCTGCTGGCGGTGGACCCCTGATGGCAT 427  
 Oy 421 GTCAACAG-AAAAAGCTGCTGACTGCGGCAATTGGCTTTGAGCGCAACGCAATANGTG 479  
 Db 428 GTCAACAGAAAAAGCTGCTGACTGCGGCAATTGGCTTTGAGCGCAACGCAATANGTG 487  
 Oy 480 CCGCGACGGGGAATTTGTTGTTGACAGACTCCGGGAGCAATGATCCCGGTAATCCT 539  
 Db 488 CCGCGACGGGGA-ANTTGTGCTGTGACAGACTCCGGGAGCAATGATCCCGGTAATCCT 546  
 Oy 540 CCGCGGGAACACTTANATACCCGCTCCTCCCAANGAAGTTGCCCTTGGGATCCCTT 599  
 Db 547 GCCCGGGGAACCTTANATACCCGCTCCTCC-ANGACGTGCCCTTGGATCACTT 602  
 Oy 600 TAAACNCAANTGAAATCTCNCCTNANGAAGAACTTTATGAACAGCTTTAANACNA 659  
 Db 603 TAAACAGCATGAAATCACTCC--AGGAAGAACTTTATGAACNCTTTAANACNA 660  
 Oy 660 TCGATGACACNCTGTCTGTCACATTTGCAATGCGCTGCTGACCAACCAATTCCT 719  
 Db 661 TCGATGACACCG--TGTCAAGTTCACATTTGCAATGCGCTGCTGACCAACCA-TTA 717  
 Oy 720 TTCGCCAACNTCTTCTCCTGCTGCTCCT-CCCAATGCAACCCGCGGAATTCCT 777

Db 718 ATCACACNTATCTATCTCATGCGCTCCACNCTCCACAAATGCAACCCACCGAATNCT 777  
 Oy 778 NTGCCCTCCCTCCCT 792  
 Db 778 TGTGCCACTCTCTT 792  
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 AB3014 727 bp DNA linear PAT 21-JAN-2000  
 LOCUS  
 DEFINITION Sequence 21 from Patent WO9853085.  
 ACCESSION AB3014  
 VERSION AB3014.1 GI:6732494  
 KEYWORDS  
 SOURCE unidentified.  
 ORGANISM unidentified.  
 REFERENCE 1 (bases 1 to 727)  
 AUTHORS Seymour, G.B. and Bird, C.R.  
 TITLE GENETIC CONTROL OF FRUIT RIPENING  
 JOURNAL Patent: WO 9853085-A 21 26-NOV-1998;  
 SEYMOUR GRAHAM BARRON (GB); ZENECA LTD (GB)  
 FEATURES Location/Qualifiers  
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 /db\_xref="taxon:32644"  
 /clone="U-139"  
 BASE COUNT 144 a 199 c 202 g 157 t 25 others  
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 Best Local Similarity 90.9%; Pred. No. 3.5e-139;  
 Matches 653; Conservative 0; Mismatches 57; Indels 8; Gaps 5;  
 Oy 1 TGTTCCTCCTTCGATCAGATCTTTTGGCTGCGAAAGCTGAGAGTGAGAGAGGCG 60  
 Db 16 TGTTCCTCCTTCGATCAGATCTTTTGGCTGCGAAAGCTGAGAGTGAGAGAGGCG 75  
 Oy 61 GCAATGACGGGGGTTTAAGATGATTCCTCTGCTTCTTCTTCTGAGGCTTCG 120  
 Db 76 GCAATGACGGGGGTTTAAGATGATTCCTCTGCTTCTTCTTCTGAGGCTTCG 135  
 Oy 121 CTGGTTTGAACGAGAGTGGGGGCTGATTTGAAGAGAGAGTCCCTGCTCGAGGAT 180  
 Db 136 CTGGTTTGAACGAGAGTGGGGGCTGATTTGAAGAGAGTCCCTGCTCGAGGAT 195  
 Oy 181 GCGGAGCATCGCGGAGGAGCTTGAAGAGAGGCTCCGCAACGCGACGCGCGATGCT 240  
 Db 196 GCGGAGCATCGCGGAGGAGCTTGAAGAGAGGCTCCGCAACGCGACGCGCGATGCT 255  
 Oy 241 TCCCTTGAAGAGAGGCTTGAACCCGCGAGCAGAAAGCCGAGTCAGACGCCCGAGAG 300  
 Db 256 TCCCTTGAAGAGAGGCTTGAACCCGCGAGCAGAAAGCCGAGTCAGACGCCCGAGAG 315  
 Oy 301 GTTGTTCGACGCTCTGTATGACATTAATCAACAGACGCTCGCATCTCTGTTAT 360  
 Db 316 GTTGTTCGACGCTCTGTATGACATTAATCAACAGACGCTCGCATCTCTGTTAT 375  
 Oy 361 CTGTGTGGGTTGACGCAACCCGATCGACGCTGCTGGCGGTGGACCCCTGATGGCAT 419  
 Db 376 CTGTGTGGGTTGACGCAACCCGATCGACGCTGCTGGCGGTGGACCCCTGATGGCAT 435  
 Oy 420 TGTCAACAGAAAAAGCTGCTGACTGCGGCAATTGGCTTTGAGCGCAACGCAATANGTG 479  
 Db 436 TGTCAACAGAAAAAGCTGCTGACTGCGGCAATTGGCTTTGAGCGCAACGCAATANGTG 495  
 Oy 480 CCGCGACGGGGAATTTGTTGTTGACAGACTCCGGGAGCAATGATCCCGGTAATCCT 539  
 Db 496 CCGCGACGGGGA-NTTGTGCTGTGACAGACTCCGGGAGCAATGATCCCGGTAATCCT 554  
 Oy 540 CCGCGGGAACACTTANATACCCGCTCCTCCCAANGAAGTTGCCCTTGGGATCCCTT 599

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Db      555  CMCGGGAAACNTTANATACGCCGTCATCC----ANGACTNCCCTCTGAGTACCTTT 610
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Db      611  TAAACNCACATGAGNATCCCGCCCA-GGAAGAATCATATATGACAGCTTTTAAACNA 669
Qy      660  TCGATGACACNCTGCTCTGCATATGGCAATGGCGCTGCTACACCAAT 717
Db      670  TCGATGAC-CCGCTGTCAGCTCNCNTTGGCAATGGGCGCTGCTCNCNTCNCNT 726

RESULT 8
A70155  A70155 727 bp DNA Linear PAT 07-MAY-1999
DEFINITION Sequence 16 from Patent WO9811228.
ACCESSION A70155
VERSION A70155.1 GI:4774570
KEYWORDS
SOURCE unidentified.
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 727)
AUTHORS Seymour G.B., Bird C.R. and Medina-Suarez, R.D.
TITLE GENETIC CONTROL OF FRUIT RIPENING
JOURNAL Patent: WO 9811228-A 16 19-MAR-1998;
FEATURES
SOURCE location/Qualifiers
1..727
/organism="unclassified"
/db_xref="taxon:32644"
/clone="U-089"

BASE COUNT 145 a 205 c 196 g 159 t 22 others
ORIGIN
Query Match 67.5% Score 543.8; DB 6; Length 727;
Best Local Similarity 86.6% Pred. No. 9.8e-12;
Matches 62; Conservative 0; Mismatches 91; Indels 6; Gaps 4;

Qy      2  GTTCTCTCTCGATCATCATCTTTTCTGCTGGAACGTGAGAGTGAGACGAGCGG 61
Db      8  GTTCTCTCTCGATCATCATCTTTTCTGCTGGAACGTGAGAGTGAGACGAGCGG 67
Qy      62  CAATGACGGCGGTTTAAGATGATTCCTCTGCTTCTTCTTCTGAGGCTTCCTGC 121
Db      68  CAATGACGGCGGTTTAAGATGATTCCTCTGCTTCTTCTTCTGAGGCTTCCTGC 127
Qy      122 TGGTTTGAACGAGGTCGGGGGTGATGGAAGCGAGAGTCTCTGGCTCGAGGATG 181
Db      128 TGGTTTGAACGAGGTCGGGGGTGATGGAAGCGAGAGTCTCTGGCTCGAGGATG 187
Qy      182 GCGGAGCATGCGGAGAGGCTTGAGAGAGCTCCGCGAACGCGACGAGCGCATCTT 241
Db      188 GCGGAGCATGCGGAGAGGCTTGAGAGAGCTCCGCGAACGCGACGAGCGCATCTT 247
Qy      242 CTTTGAAGAGAGGCTGTAAACCGGAGCAGAACGCCGAGTCGACAGACCCGAGAGG 301
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Qy      302 TTTCTTGAAGAGGCTGTAAACCGGAGCAGAACGCCGAGTCGACAGATCTTGGTATC 361
Db      308 TTTCTTGAAGAGGCTGTAAACCGGAGCAGAACGCCGAGTCGACAGATCTTGGTATC 367
Qy      362 TGTGTCGCGGTTCAAGGCAACCGATGACAGCTGTGCGGTGCGACCTGATTTGGCATG 421
Db      368 TGTGTCGCGGTTCAAGGCAACCGATGACAGCTGTGCGGTGCGACCTGATTTGGCATG 427
Qy      422 TCAACGAAAAAGCTGTGACTGCGGCAATTTGGCTTTGG-ACGCAACGCAATANGTGC 480
Db      428 TCAACGAAAAAGCTGTGACTGCGGCAATTTGGCTTTGG-ACGCAACGCAATANGTGC 487
Qy      481 CCGAGAGGGAATTTGTTGTTGAGACAGACTCGGGGACNATGATCCCGTGAATCTTC 540
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Qy      541  GCCGGGAACACTTANATACCCGCTCNCNANGAAGTTGCCCTCTGGGATCCCTTT 600
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Qy      601  AAACNCNANTGGAATCTCNCNTCNANGAAGAAGCTNTATGACAGCTTTTAAACNAT 660
Db      604  AAACGACATTTGGA-ATCNCCTCCGGAAGACTCTTTTAAACGCTTTNNAACATC 662
Qy      661  CGATGACNCTGCTCTGCTGTCACATTTGCCAATGGGCGCTGCTACACCAATTCN 720
Db      663  NATGACNCTGCTCAGCTTCTCCACNTTTCACATTTGCCAATGGGCGCTGCTCNCNANTTTAA 722
Qy      721  TCCCC 725
Db      723  TCNCC 727

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DEFINITION Sequence 18 from Patent WO9811228.
ACCESSION A70157
VERSION A70157.1 GI:4774572
KEYWORDS
SOURCE unidentified.
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 724)
AUTHORS Seymour G.B., Bird C.R. and Medina-Suarez, R.D.
TITLE GENETIC CONTROL OF FRUIT RIPENING
JOURNAL Patent: WO 9811228-A 18 19-MAR-1998;
FEATURES
SOURCE location/Qualifiers
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BASE COUNT 143 a 201 c 197 g 155 t 28 others
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Query Match 66.5% Score 536; DB 6; Length 724;
Best Local Similarity 89.7% Pred. No. 1.1e-12;
Matches 61; Conservative 0; Mismatches 62; Indels 9; Gaps 5;

Qy      6  TCTCTTGAATCATCTTTTCTGCTGGAACGTGAGAGTGAGACGAGGCGCAAT 65
Db      9  TCTCTTGAATCATCTTTTCTGCTGGAACGTGAGAGTGAGACGAGGCGCAAT 68
Qy      66  GACGGCGGTTTAAGATGATTCCTCTGCTTCTTCTTCTGAGGCTTCCTGCTGT 125
Db      69  GACGGCGGTTTAAGATGATTCCTCTGCTTCTTCTTCTTATGAGGCTTCCTGCTGT 128
Qy      126 TTTGAACGAGGTCGGGGGTGATTTGAACGAGAGTCTCTGCTGCGAGAAATGGCGG 185
Db      129 TTTGAACGAGGTCGGGGGTGATTTGAACGAGAGTCTCTGCTGCGAGAAATGGCGG 188
Qy      186 AGCATGCGGAGAGCTTTGAGAGAGGCTCCGCGAACGCGACGAGCGCATCTTCTT 245
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Qy      246 GGAAGAGGCTGTAAACCGGAGCAGAACGCCAGTCGACGACCCGAGAGGTTGC 305
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Qy      306 TTTGAGGCTCTGATGACCAATTAACACAGAGGCTGCGAGATCTTGTATCTGTC 365
Db      309 TTTGAGGCTCTGATGACCAATTAACACAGAGGCTGCGAATCTTGTATCTGTC 368
Qy      366 GTGCGGTTCAAGGCAACCGATGACAGCTGTGCGGTGCGACCTGATTTGGATGCA 425
Db      369 GTGCGGTTCAAGGCAACCGATGACAGCTGTGCGGTGCGACCTGATTTGGATGCA 428

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Db 307 TTGCTTGACGGTCTCTACGACCATATATACAGACAGCGCTCCGACATCTCTTGATTATC 366
QY 362 TGTGTCGCGGTTTCAGGCA--CCCGATGAGACACTGTGGCGTG--CGACCCCTGATTGCA 419
Db 367 TGTGTCGCGGTTTCAGGCAACCCGATGAGACACTGTGGCGTG--CGACCCCTGATTGCA 426
QY 420 TGTACACAGAAAAAGCTGCTGACTGCGGCACTTGGC--TTTGACGCGAAGCCGATGATG 478
Db 427 TGTACACAGAAAAAGCTGCTGACTGCGGCACTTGGC--TTTGACGCGAAGCCGATGATG 486
QY 479 GCGGC--GACGGGGAATTTGTGCTG--TGACAGACTG--GGGACGATGATGCGCGTGA 534
Db 487 GCGGCACCGCGGAGGATTTGCTGCTTGTGACACTGCGGAGGACATGATGCTCCGTA 546
QY 535 ATCTGCGCC--GGGACACTTANATATACCCGCTGCTCCGATGAGATGTCCTGCGA 592
Db 547 ATCTGCGCCCGCGGAGGACACTTANATATGCTGCTGATGAGATGTCCTGCGA 603
QY 593 TCCGCTTTAAACGCAATGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 652
Db 604 TCCGCTTTAAACGCAATGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 661
QY 653 AANACNATGATGAGCAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 697
Db 662 AANACATCTCAATGAGCAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 706

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RESULT 12  
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LOCUS Oryza sativa chromosome 4 clone OSJNBa0095E20, \*\*\* SEQUENCING IN  
PROGRESS \*\*\*, 4 ordered pieces.  
AL731627 2 GI:21743085  
ACCESSION AL731627  
VERSION HTG: HTGS\_PHASE2.  
KEYWORDS Oryza sativa.  
SOURCE Oryza sativa.  
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Eriophoraceae; Oryzaceae; Oryza.

## REFERENCE

1 Han, B., Feng, Q., Huang, Y. C., Li, Y., Zhu, J. J., Zhao, Q., Hu, X.,  
Liu, Y. L., Wu, J., Yu, Z., Chen, L., Fan, D. L., Wang, Q. J., Zhang, L.,  
Lu, Y. Q., Yu, S. L., Liu, X. H., Lu, T. T., Zhang, Y. J., Lu, Y., Li, C.,  
Li, T., Zhang, Y., Hu, H., Jia, P. X., Qian, Y. M., Ying, K., Zhou, B.,  
Chen, Z. H., Hao, P., Zhang, L., Wu, M., Zhang, R. Q., Guan, J. P., Fu, G.,  
Wang, S. Y., Ren, S. X., Lv, G., Lin, W., Gu, W. Q., Zhu, G. F., Tu, Y. F.,  
Jia, J., Yin, H. F., Zhang, Y., Cai, Z., Chen, J., Kang, H., Chen, X. Y.,  
Shao, C. Y., Sun, Y., Hu, Q. P., Zhang, X. L., Zhang, W., Wang, L. J.,  
Ding, C. W., Sheng, H. H., Gu, J. L., Chen, S. T., Ni, L., Zhu, F. H. and  
Hong, G. F.

## TITLE

Submitted (27-JUN-2002) Han Bin, National Center for Gene Research,  
Chinese Academy of Sciences, 500# Cao Bao Road, Shanghai 200233,  
CHINA. E-mail enquiries: bhan@ncgr.ac.cn. Clone requests:  
bhan@ncgr.ac.cn

## REMARK

Oryza sativa japonica (nipponbare) genomic DNA, chromosome 4, BAC  
clone: OSJNBa0095E20.  
On Jul 12, 2002 this sequence version replaced gi:20452125.

## COMMENT

Web site: http://www.ncgr.ac.cn  
----- Summary Statistics  
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Assembly program: phrap

NOTE: This is a PHASE2 sequence. Gaps are shown by nnnn. Genes  
were identified by a combination of several methods: Gene  
prediction programs including Egenes (http://www.softberry.com/),  
genescan (http://CCR-081.mt.edu/GENSCAN.html), GenesMark-ES (http://  
http://genemark.biology.gatech.edu/Genemark/), tRNAscan-SE (Sean  
Eddy, http://genome.wustl.edu/eddy/tRNAscan-SE/), searches of the  
complete sequence against NCBI non-redundant protein database (nr)  
(ftp://ncbi.nlm.nih.gov/blast/db) and the EST database at NCGR.  
\* NOTE: This is a 'working draft' sequence. It currently  
consists of 4 contigs. Gaps between the contigs

\* are represented as runs of N. The order of the pieces  
\* is believed to be correct as given, however the sizes  
\* of the gaps between them are based on estimates that have  
\* provided by the submitter.  
\* This sequence will be replaced  
\* by the finished sequence as soon as it is available and  
\* the accession number will be preserved.  
\* 1 82614: contig of 82614 bp in length  
\* 82615 82814: gap of 200 bp  
\* 82815 84736: contig of 1922 bp in length  
\* 84737 84936: gap of 200 bp  
\* 84937 93650: contig of 8714 bp in length  
\* 93651 93850: gap of 200 bp  
\* 93851 127202: contig of 33352 bp in length.  
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/variety="Nipponbare"  
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BASE COUNT 37100 a 25341 c 26047 g 37309 t 605 others  
ORIGIN

Query Match 21.6%; Score 174.4; DB 2; Length 127202;  
Best Local Similarity 68.0%; Pred. No. 7.6e-35;  
Matches 299; Conservative 0; Mismatches 133; Indels 8; Gaps 5;

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QY 374 CAGGACCCGATGAGACAGCTGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 433
Db 52049 CCGGCAATCCGATGAGACAGCTGCTGAGAGTGCGGCGGCGGCGGCGGCGGCGG 51990
QY 434 AGCTGCTGACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 493
Db 51989 GCGTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 51931
QY 494 TTGCTGCTGACAGACCTCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 553
Db 51930 ATCTACCTGCTGACAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 51872
QY 554 TAAATACCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 613
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QY 614 AATCTGCTGCAATGAGACAGCTTATGACAGCTTATGACAGCTTATGACAGCTTAT 673
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## RESULT 13

AY085026 1633 bp mRNA linear PLN 21-JUN-2002  
DEFINITION Arabidopsis thaliana clone 124816 mRNA, complete sequence.  
ACCESSION AY085026  
VERSION AY085026.1 GI:21403736  
KEYWORDS FLI cDNA.  
SOURCE thale cress.  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;



Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

1 (bases 1 to 1633)  
Haas,B.J., Volfovsky,N., Town,C.D., Troukhan,M., Alexandrov,N., Feldmann,K.A., Flavell,R.B., White,O., and Salzberg,S.L.  
Full-length messenger RNA sequences greatly improve genome annotation  
Genome Biol. (2002) In press

2 (bases 1 to 1633)  
Brover,V., Troukhan,M., Alexandrov,N., Lu,Y.-P., Flavell,R. and Feldmann,K.  
Full-length cDNA from Arabidopsis thaliana  
Unpublished  
3 (bases 1 to 1633)  
Brover,V., Troukhan,M., Alexandrov,N., Lu,Y.-P., Flavell,R. and Feldmann,K.  
Direct Submission  
Submitted (11-MAR-2002) Ceres, Inc, 3007 Malibu Canyon Road, Malibu, CA 90265, USA

This clone sequence is one of 5,000 Ceres full-length cDNAs made available to TIGR and Genbank. The following quality assessment of this set was done by comparison with known proteins: two percent of the clones are estimated to be 5'-truncated; less than one percent are 3'-truncated; approximately two percent represent alternative splice variants, including unspliced introns and spliced exons; one percent may contain premature stop codons; five percent may have frame shifts in a coding region. A sequence is considered to be 5'-truncated if it lacks the translation initiation start (ATG). A sequence is considered to be 3'-truncated if it lacks the C-terminal end of the encoded protein. Please note that these cDNA sequences are derived from the Ms or laer ecotypes and therefore may contain polymorphisms when compared to sequences from Col-0. Genset carried out the library production and sequencing of the full-length clones. Ceres, Inc, carried out the clustering of the 5' sequences, selection of clones, and sequence assembly.

FEATURES  
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COMMENT

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complete sequence.  
AC016827  
AC016827.7 GI:12408743  
HTG.  
Arabidopsis thaliana.  
Arabidopsis thaliana.  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
1 (bases 1 to 90142)  
Lin,X., Kaul,S., Town,C.D., Benito,M.-I., Creasy,T.H., Haas,B.,  
Wu,D., Ronning,C.M., Koo,H., Fujii,C.Y., Uteckack,T.R.,  
Barnstead,M.E., Bowman,C.L., White,O., Nierman,W.C. and Fraser,C.M.  
Arabidopsis thaliana chromosome III BAC F17A9 genomic sequence  
Unpublished  
2 (bases 1 to 90142)  
Lin,X. and Kaul,S.  
Direct Submission  
Submitted (08-DEC-1999) The Institute for Genomic Research, 9712  
Medical Center Dr., Rockville, MD 20850, USA, xlinet@tigr.org  
3 (bases 1 to 90142)  
Lin,X.  
Direct Submission  
Submitted (24-JAN-2001) The Institute for Genomic Research, 9712  
Medical Center Dr., Rockville, MD 20850, USA  
On Jan 24, 2001 this sequence version replaced gi:12280775.  
Address all correspondence to:at@tigr.org

BAC clone F17A9 is from Arabidopsis chromosome III and is near the  
molecular marker m1357.  
The orientation of the sequence is from SP6 to T7 end of the BAC  
clone.  
Genes were identified by a combination of three methods: Gene  
prediction programs including GRAFT (available by anonymous ftp  
from arthur.epm.ornl.gov), Genefinder (Phil Green, University of  
Washington), Genscan (Chris Burge,  
http://genomic.stanford.edu/~chris/GENSCANW.html), and NetPlantGene  
(http://www.cds.dtu.dk/netgene/chsnetgene.html), searches of the  
complete sequence against a peptide database and the Arabidopsis  
EST database at TIGR (http://www.tigr.org/tidb/at.html).  
Annotated genes are named to indicate the level of evidence for  
their annotation. Genes with similarity to other proteins are named  
after the database hits. Genes without significant peptide  
similarity but with EST similarity are named as 'unknown' proteins.  
Genes without protein or EST similarity, that are predicted by more  
than two gene prediction programs over most of their length are  
annotated as 'hypothetical' proteins. Genes encoding tRNAs are  
predicted by tRNAscan-SE (Sean Eddy,  
http://genome.wustl.edu/eddy/tRNAscan-SE/). Simple repeats are

identified by repeatmasker (Arian Smil,  
http://ftp.genome.washington.edu/RM/RepeatMasker.html).

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Best Local Similarity 63.5%; Pred. No. 5.6e-29;

Matches 277; Conservative 0; Mismatches 152; Indels 7; Gaps 4;

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OY 617 TCTCCTCANGAAGAACTCTTATGAACAGCTTTAANANANGATGAGCNCNGTGC 676  
DB 53180 TAAAC-CTTGAAACGAAGAGCTGATCAAGACCTTCAAAACATGATGCTGTGTC 53122  
OY 677 CTCGTCACATTCGCAATGCGCGCTGCGCTCACCACCAATTTCTCCACNTCTTCT 736  
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ACCESSION A83003  
VERSION A83003.1 GI:6732483  
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SOURCE unidentified.  
ORGANISM unidentified.  
REFERENCE 1 (bases 1 to 823)  
AUTHORS Seymour,G.B. and Bird,C.R.  
TITLE GENETIC CONTROL OF FRUIT RIPENING  
JOURNAL Patent: WO 9853085-A 10 26-NOV-1998;  
SEYMOUR GRAHAM BARROW (GB); ZENECA LTD (GB)  
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DB 197 GCAGACCTCTGCGGCTGCGATCTGAGTGGGCCGACACACCGGACGCGCTCGCGACTG 256  
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Job time : 1557 secs



GenCore version 5.1.6  
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Run on: June 19, 2003, 11:17:55 ; Search time 181 Seconds  
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**Pred. NO.** is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

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	4	588.8	73.1		793	20	AAV69447	Banana fruit ripen
	5	572.2	71.0		727	20	AAV69440	Banana fruit ripen
	6	543.8	67.5		727	19	AAV28658	Ripening banana pu
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	8	510.8	63.4		704	20	AAV69446	Banana fruit ripen
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21	130.4	16.2	1323	21	AAC51583	Arabidopsis thaliana
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29	120.8	15.0	1359	21	AAC50766	Arabidopsis thaliana
30	119.4	14.8	710	20	AAV69453	Banana fruit ripen
31	118.4	14.7	1413	21	AAC51079	Arabidopsis thaliana
32	116.4	14.4	1257	21	AAC42899	Arabidopsis thaliana
33	116.4	14.4	1317	21	AAC50549	Arabidopsis thaliana
34	114.6	14.2	1514	21	AAC41053	Arabidopsis thaliana
35	113	14.0	1615	21	AAC51025	Arabidopsis thaliana
36	113	14.0	1617	21	AAC41994	Arabidopsis thaliana
37	110.4	13.7	1221	21	AAC47293	Arabidopsis thaliana
38	110.4	13.7	1631	21	AAC33659	Arabidopsis thaliana
39	109.4	13.7	1631	21	AAC49928	Arabidopsis thaliana
40	109.6	13.6	1125	21	AAC42903	Arabidopsis thaliana
41	94	11.7	438	21	AAA31518	Plant microateellu
42	93.4	11.6	460	24	AB193674	Arabidopsis thaliana
43	83.4	10.3	1807	21	AAC51305	Arabidopsis thaliana
44	83.4	10.3	1812	21	AAC39116	Arabidopsis thaliana
45	81.8	10.1	1523	21	AAC51573	Arabidopsis thaliana

## ALIGNMENTS

RESULT 1	-
AAV28655	
ID	AAV28655 standard; cDNA; 806 BP

AC AAV28655

DT 29-JUL-1998 (first entry)

DE Ripening banana pulp cDNA clone U-U68 SEQ ID NO:13.

KW Banana, ripening; pulp; *Musa acuminata* cv. Grand Nain; fruit, genetic control; tissue senescence; ss.

Musa acuminata.

PN W09811228-A2.

PD 19-MAR-1998.

PF 08-SEP-1997;  
yy

PR	25-APR-1997;	97GB-0008366.
PR	10-SEP-1996;	96GB-0018862

PA (ZENEC) ZENEC LTD.

AA Bird CR, Medina-Suarez RDJ, Seymour GB;  
PI

WPI; 1998-207389/18

PT Modulation of ripening or tissue senescence in bananas - comprises

PT use of DNA isolated from ripening banana pulp to produce genetically

PT modified fruit  
 XX  
 PS Claim 1; Page 26; 72pp; English.  
 XX  
 CC The present sequence represents a cDNA clone isolated from ripening  
 CC banana pulp. 57 clones were isolated and are given in AAV28643 to  
 CC AAV28699. The cDNA clone sequences can be used in a method of modulating  
 CC ripening or tissue senescence processes in plants of the genus *Musa*. The  
 CC method comprises: (a) inserting into the plant material at least 1 of the  
 CC 57 sequences (as above); (b) regenerating the plant material, and (c)  
 CC selecting from the transformed regenerants, plants with modulated  
 CC ripening or tissue senescence characteristics. Also described in the  
 CC present invention are: (1) plants, their progeny, seed and material  
 CC obtained from the plants, produced by the above method; (2) a vector  
 CC functional in plants comprising a promoter region which is operably in  
 CC plant cells, a polynucleotide sequence as defined above, and a  
 CC transcription termination sequence; and (3) a method of controlling  
 CC plant pathogens comprising the application of anti-pathogenic agent to  
 CC plants of (1).  
 XX  
 SQ Sequence 806 BP; 157 A; 229 C; 212 G; 180 T; 28 other;

Query Match 96.5%; Score 778; DB 19; Length 806;  
 Best Local Similarity 100.0%; Pred. No. 1e-221;  
 Matches 806; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTTCCTCTTCGATCACAATCTTTTGTCTGTGGAAACGTGAGAGTGAGAGAGCG 60  
 DB 1 TGTTCCTCTTCGATCACAATCTTTTGTCTGTGGAAACGTGAGAGTGAGAGAGCG 60  
 QY\* 61 GCATATGACGGGGGTTTAAAGATGATTCCTCTCTCTCTCTCTCTCTCTCTCTCT 120  
 DB 61 GCATATGACGGGGGTTTAAAGATGATTCCTCTCTCTCTCTCTCTCTCTCTCTCT 120  
 QY 121 CTGCTTTTGAAGCGAGGTGCGGGGTGGATTTGAAGCGAGAGGTCCTCTGCTGAGGAAT 180  
 DB 121 CTGCTTTTGAAGCGAGGTGCGGGGTGGATTTGAAGCGAGAGGTCCTCTGCTGAGGAAT 180  
 QY 181 GCGGAGCATCGCGAGAGGCTTGAGAGAGGCTCCGCGAAGCGAGCGAGCGGATGCT 240  
 DB 181 GCGGAGCATCGCGAGAGGCTTGAGAGAGGCTCCGCGAAGCGAGCGAGCGGATGCT 240  
 QY 241 TCCTTGGAGAGAGGGCTGTAAACCCGGGAGAGAGAGCGGAGTGCAGACCCCGAGAG 300  
 DB 241 TCCTTGGAGAGAGGGCTGTAAACCCGGGAGAGAGAGCGGAGTGCAGACCCCGAGAG 300  
 QY 301 GTTGCTTCGACGCTCCGATGACCATTAATCAACAGACGCTGGGAGATCTTGGTTAT 360  
 DB 301 GTTGCTTCGACGCTCCGATGACCATTAATCAACAGACGCTGGGAGATCTTGGTTAT 360  
 QY 361 CTGTGCTGGGTTCAAGCAACCCGATCGAGAGTGTGGGAGTGCAGACCTGATTTGGCAT 420  
 DB 361 CTGTGCTGGGTTCAAGCAACCCGATCGAGAGTGTGGGAGTGCAGACCTGATTTGGCAT 420  
 QY 421 GTCAACAGAAAAAGCTCGCTGACTGCGGATTTGGCTTTGAGAGCAACGNAATANGTGGC 480  
 DB 421 GTCAACAGAAAAAGCTCGCTGACTGCGGATTTGGCTTTGAGAGCAACGNAATANGTGGC 480  
 QY 481 CGGAGCGGGAATTTGTCTGTGACAGACTCCGGGAGACATGATCCCGGATATCTTC 540  
 DB 481 CGGAGCGGGAATTTGTCTGTGACAGACTCCGGGAGACATGATCCCGGATATCTTC 540  
 QY 541 GCCCGGGAACACTTANATACCCGCTNTCCAAANGAAGTTGCCCTCTGGGATCCCTTT 600  
 DB 541 GCCCGGGAACACTTANATACCCGCTNTCCAAANGAAGTTGCCCTCTGGGATCCCTTT 600  
 QY 601 AAACNANANTGAAATCTCNCTCNANGAAGAGACTCATTATGAAAGCTTTAANCMAT 660  
 DB 601 AAACNANANTGAAATCTCNCTCNANGAAGAGACTCATTATGAAAGCTTTAANCMAT 660  
 QY 661 CGATGACNCGNGTCTCTGTCACATTTGCAATGGCGGCTGNTACCAACCAATTTTCN 720  
 DB 661 CGATGACNCGNGTCTCTGTCACATTTGCAATGGCGGCTGNTACCAACCAATTTTCN 720

QY 721 TCCCAACNTCTTCTTCNTNGCCTCCNCTCCCAATGCAACCCCGGGAATTCCTNGT 780  
 DB 721 TCCCAACNTCTTCTTCNTNGCCTCCNCTCCCAATGCAACCCCGGGAATTCCTNGT 780  
 QY 781 CCCCNCTCCCTTCTCTATGATNG 806  
 DB 781 CCCCNCTCCCTTCTCTATGATNG 806

RESULT 2  
 AAV69457  
 ID AAV69457 standard; cDNA; 748 BP.  
 XX  
 AC AAV69457;  
 XX  
 DT 15-MAR-1999 (first entry)  
 XX  
 DE Banana fruit ripening-related clone U-113 cDNA.  
 XX  
 KM Fruit ripening; banana; modulator; tissue senescence; crop; plant;  
 KW triploid; plant breeding; ss.  
 XX  
 OS *Musa acuminata*.  
 XX  
 PN WO9853085-A1.  
 XX  
 PD 26-NOV-1998.  
 XX  
 PF 05-MAY-1998; 98WO-GB01297.  
 XX  
 PR 20-MAY-1997; 97GB-0010370.  
 XX  
 PA (ZENEC) ZENEC LTD.  
 XX  
 PI Bird CR, Medina-Suarez RDJ, Seymour GB;  
 XX  
 DR WPI; 1999-059745/05.  
 XX  
 PT New method of modulating fruit ripening or tissue senescence  
 PT characteristics of *Musa* plants - by introducing DNA sequences,  
 PT useful in processes for modifying plant/fruit ripening  
 PT characteristics  
 PS  
 XX  
 CC Claim 1; Page 29; 78pp; English.  
 CC AAV69440-V69512 are cDNA sequences which are used in a method to  
 CC modulate the fruit ripening or tissue senescence characteristics of *Musa*  
 CC *acuminata* (banana) plants. The method provides a recombinant way of  
 CC modulating ripening/senescence characteristics of bananas, which are a  
 CC globally important crop. In particular, the method can modulate such  
 CC characteristics in the desert banana, which due to its triploid nature  
 CC is unaffected by conventional plant breeding techniques.  
 XX  
 SQ Sequence 748 BP; 154 A; 211 C; 206 G; 163 T; 14 other;

Query Match 73.4%; Score 591.8; DB 20; Length 748;  
 Best Local Similarity 91.7%; Pred. No. 3.4e-166;  
 Matches 664; Conservative 0; Mismatches 52; Indels 8; Gaps 4;

QY 1 TGTTCCTCTTCGATCACAATCTTTTGTCTGTGGAAACGTGAGAGTGAGAGAGCG 60  
 DB 1 TGTTCCTCTTCGATCACAATCTTTTGTCTGTGGAAACGTGAGAGTGAGAGAGCG 75  
 QY 61 GCATATGACGGGGGTTTAAAGATGATTCCTCTCTCTCTCTCTCTCTCTCTCTCT 120  
 DB 61 GCATATGACGGGGGTTTAAAGATGATTCCTCTCTCTCTCTCTCTCTCTCTCTCT 135  
 QY 121 CTGCTTTTGAAGCGAGGTGCGGGGTGGATTTGAAGCGAGAGTCTCTGGCTGAGGAAT 180  
 DB 121 CTGCTTTTGAAGCGAGGTGCGGGGTGGATTTGAAGCGAGAGTCTCTGGCTGAGGAAT 195  
 QY 136 CTGCTTTTGAAGCGAGGTGCGGGGTGGATTTGAAGCGAGAGTCTCTGGCTGAGGAAT 195  
 DB 136 CTGCTTTTGAAGCGAGGTGCGGGGTGGATTTGAAGCGAGAGTCTCTGGCTGAGGAAT 240

DB 196 GCGGAGCATCGCGAGGAGCTTGAGAGAGGCTCCGCAAGCGACGACCGCATGCT 255  
QY 241 TCCCTTGGAAGAGAGGCTCTAAACCCGGGAGCAGAAAGCCGACGTGACGACACCCCGAGAG 300  
DB 256 TCCCTTGGAAGAGAGGCTCTAAACCCGGGAGCAGAAAGCCGACGTGACGACACCCCGAGAG 315  
QY 301 GTTGTGTCGAGCGCTCTGTGACCATTAATCAACAGACGCGCGGATCTCTGTAT 360  
DB 316 GTTGTGTCGAGCGCTCTGTGACCATTAATCAACAGACGCGCGGATCTCTGTAT 375  
QY 361 CTGTGTCGCTTCAAGCAGACCCGATCGACGACTGTGCGGTGCGACCCGTGATTTGGCAT 420  
DB 376 CTGTGTCGCTTCAAGCAGACCCGATCGACGACTGTGCGGTGCGACCCGTGATTTGGCAT 435  
QY 421 GTCAACAGAAAAAGCTCGCTACTGCGGCGATTTGGCTTTGAGCAGCAACGATANGTGGC 480  
DB 436 GTCAACAGAAAAAGCTCGCTACTGCGGCGATTTGGCTTTGAGCAGCAACGATANGTGGC 495  
QY 481 CGCGAGCGGGAATTTGTTGTTGTGACGACTCCGGGAGCAGATCCCGGATCCGATTCCTC 540  
DB 496 CGCGAGCGGGAATTTGTTGTTGTGACGACTCCGGGAGCAGATCCCGGATCCGATTCCTC 555  
QY 541 GCGCGGGAACACTTANATACCCGTCNTCCAAAGAGTGGCCCTCTGTGGATCCCTTT 600  
DB 556 CCGCGGAACACTTANATACCCGTCNTCCAAAGAGTGGCCCTCTGTGGATCCCTTT 610  
QY 601 AAACNCNANTGGAATCTCNCNTCNANGAAGAACCTTATGAACAGCTTTAANACNAT 660  
DB 611 AAACNCNANTGGAATCTCNCNTCNANGAAGAACCTTATGAACAGCTTTAANACNAT 669  
QY 661 CGATGAGCNCNGTTCCTGCTGCACATTCGCAATGGCGCTGCTGCAACCAATTCN 720  
DB 670 CGATGAGC-CGCTGTTCACTCCACTTTGCCAATGSC-CCTGCTGCACTCCANTNCT 727  
QY 721 TCCG 724  
DB 728 CACG 731

RESULT 3  
AAV69450  
ID AAV69450 standard; cDNA: 745 BP.  
AC AAV69450;  
XX 15-MAR-1999 (first entry)  
DE Banana fruit ripening-related clone U-52 cDNA.  
KW Fruit ripening; banana; modulator; tissue senescence; crop; plant;  
KM triploid; plant breeding; SS.  
XX Musa acuminate.  
OS WO9853085-A1.  
XX 26-NOV-1998.  
PF 05-MAY-1998; 98WO-GB01297.  
PR 20-MAY-1997; 97GB-0010370.  
XX (ZENBE) ZENBECA LTD.  
XX Bird CR, Medina-Suarez RDJ, Seymour GB;  
PI WPI: 1999-059745/05.  
DR New method of modulating fruit ripening or tissue senescence  
PT characteristics of Musa plants - by introducing DNA sequences,  
PT useful in processes for modifying plant/fruit ripening  
PT characteristics

XX PS Claim 1; page 24-25; 78pp; English.  
CC AAV69440-v69512 are cDNA sequences which are used in a method to  
CC modulate the fruit ripening or tissue senescence characteristics of Musa  
CC acuminate (banana) plants. The method provides a recombinant way of  
CC modulating ripening/senescence characteristics of bananas, which are a  
CC globally important crop. In particular, the method can modulate such  
CC characteristics in the dessert banana, which due to its triploid nature  
CC is unaffected by conventional plant breeding techniques.  
XX SQ Sequence 745 BP; 153 A; 204 C; 203 G; 163 T; 22 other;  
Query Match 73.3%; Score 591.2; DB 20; Length 745;  
Best Local Similarity 90.5%; Pred. No. 5.2e-166;  
Matches 673; Conservative 0; Mismatches 61; Indels 10; Gaps 5;  
QY 1 TGTTCCTCTTCGATCAGATCTTTTGTCTGGAAGACGTGAGAGTGAAGAGGCG 60  
DB 7 TGTTCCTCTTCGATCAGATCTTTTGTCTGGAAGACGTGAGAGTGAAGAGGCG 66  
QY 61 GCAATGACGCGGCTTTAAGATGATCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120  
DB 67 GCAATGACGCGGCTTTAAGATGATCTCTCTCTCTCTCTCTCTCTCTCTCTCT 126  
QY 121 CTGTGTTGAACGAGGCTGCGGGGTGATGGAAGAGAGAGGCTCTGCGAGGAT 180  
DB 127 CTGTGTTGAACGAGGCTGCGGGGTGATGGAAGAGAGGCTCTGCGAGGAT 186  
QY 181 GCGGAGCAGTCGCGGAGGAGCTTGAAGAGAGGCTCGCGAAGCGACGCGCATGCT 240  
DB 187 GCGGAGCAGTCGCGGAGGAGCTTGAAGAGAGGCTCGCGAAGCGACGCGCATGCT 246  
QY 241 TCCCTTGGAAGAGAGGCTGTAAACCCGGGAGCAGAAAGCCGACGTGAGAGACCCCGAGAG 300  
DB 247 TCCCTTGGAAGAGAGGCTGTAAACCCGGGAGCAGAAAGCCGACGTGAGAGACCCCGAGAG 306  
QY 301 GTTGTGTCGAGCGCTCTGTGACCATTAATCAACAGACGCGGATCCGATTCCTG 360  
DB 307 GTTGTGTCGAGCGCTCTGTGACCATTAATCAACAGACGCGGATCCGATTCCTG 366  
QY 361 CTGTGTCGCTTCAAGCAGACCCGATCGACGACTGTGCGGTGCGACCCGTGATTTGGCAT 420  
DB 367 CTGTGTCGCTTCAAGCAGACCCGATCGACGACTGTGCGGTGCGACCCGTGATTTGGCAT 426  
QY 421 GTCAACAG-AAAAAAGCTCGTACTGCGGCAATTTGGCTTTGAGCAGCAACGATANGTGG 479  
DB 427 GTCAACAGAAAAAAGCTCGTACTGCGGCAATTTGGCTTTGAGCAGCAACGATANGTGG 486  
QY 480 CGCGAGCGGGAATTTGTTGTTGTGACGACTCCGGGAGCAGATCCCGGATTCCT 539  
DB 487 CGCGAGCGGGAATTTGTTGTTGTGACGACTCCGGGAGCAGATTCCTG 544  
QY 540 CGCGAGCGGGAATTTGTTGTTGTGACGACTCCGGGAGCAGATTCCTG 599  
DB 545 CMC CGCGGGAACNCTTANATAGCGGCTGATC-----ANGACGTGCCCTGTGATCAGCTT 600  
QY 600 TAAACNCNANTGGAATCTCNCNTCNANGAAGAACCTTATGAACAGC---TTTANA 656  
DB 601 TAAACNCNANTGGAATCTCNCNTCNANGAAGAACCTTATGAACAGC---TTTANA 660  
QY 657 CNAATGATGAGCNCNGTCTGCTGTCACATTCGCAATGGCGGCTGCAACCAACAT 716  
DB 661 ACATGATGAGCNCNGTCTGCTGTCACATTCGCAATGGCGGCTGCAACCAACAT 720  
QY 717 TTCNTCCCAACNCTTTCTTCNT 740  
DB 721 TACATCAACAGCTATCTCCAT 744

RESULT 4  
AAV69447  
ID AAV69447 standard; cDNA: 793 BP.



XX AAV69447;  
 AC 15-MAR-1999 (first entry)  
 DT XX  
 DE Banana fruit ripening-related clone U-22 cDNA.  
 KW Fruit ripening; banana; modulator; tissue senescence; crop; plant;  
 KM triploid; plant breeding; ss.  
 OS Musa acuminata.  
 XX W09853085-A1.  
 PN 26-NOV-1998.  
 PD 05-MAY-1998; 98MO-GB01297.  
 PF 20-MAY-1997; 97GB-0010370.  
 PR (ZENNE ) ZENNECA LTD.  
 PA Bird CR, Medina-Suarez RDJ, Seymour GB;  
 XX WPI; 1999-059745/05.  
 DR New method of modulating fruit ripening or tissue senescence  
 XX characteristics of Musa plants - by introducing DNA sequences,  
 PT useful in processes for modifying plant/fruit ripening  
 PT characteristics  
 XX Claim 1; Page 22-23; 78pp; English.  
 PS AAV69440-V69512 are cDNA sequences which are used in a method to  
 CC modulate the fruit ripening or tissue senescence characteristics of Musa  
 CC acuminate (banana) plants. The method provides a recombinant way of  
 CC modulating ripening/senescence characteristics of bananas, which are a  
 CC globally important crop. In particular, the method can modulate such  
 CC characteristics in the dessert banana, which due to its triploid nature  
 CC is unaffected by conventional plant breeding techniques.  
 XX  
 SO Sequence 793 BP; 170 A; 222 C; 215 G; 171 T; 15 other;  
 Query Match 73.1%; Score 588.8; DB 20; Length 793;  
 Best Local Similarity 88.7%; Pred. No. 2.8e-165;  
 Matches 705; Conservative 0; Mismatches 77; Indels 13; Gaps 7;  
 QY 1 TGTTCCTCTCTGATCACAATCTTTGCTCTGGAACCTGAGAGTGAAGAGGCG 60  
 DB 8 TGTTCCTCTCTGATCACAATCTTTGCTCTGGAACCTGAGAGTGAAGAGGCG 67  
 QY 61 GCAATGACGCGGGTTTAAGATGATTCCTCTCTGCTTCTTCTTCTTCTTCTTCT 120  
 DB 68 GCAATGACGCGGGTTTAAGATGATTCCTCTCTGCTTCTTCTTCTTCTTCTTCT 127  
 QY 121 CTGCTTTGAACGAGGCTCGGGGCTGATTTGAAGCGAGAGTCTCTGCTCGAGCAAT 180  
 DB 128 CTGCTTTGAACGAGGCTCGGGGCTGATTTGAAGCGAGAGTCTCTGCTCGAGCAAT 187  
 QY 181 GGGGAGCATCGGGGAGGAGCTTGAGAGAGGCTCGCGGAACCGGACGACCGGATGCT 240  
 DB 188 GGGGAGCATCGGGGAGGAGCTTGAGAGAGGCTCGCGGAACCGGACGACCGGATGCT 247  
 QY 241 TCCCTGGAAGAGAGGCTGTAACCGGAGAGAGCGCAATGAGAGCGGCGGAGAG 300  
 DB 248 TCCCTGGAAGAGAGGCTGTAACCGGAGAGCGCAATGAGAGCGGCGGAGAG 307  
 QY 301 GTTCTTCGACGGTCTGTGATGACCATTAATCAACAGACGGCTGCGAGATCTTGTAT 360  
 DB 308 GTTCTTCGACGGTCTGTGATGACCATTAATCAACAGACGGCTGCGAGATCTTGTAT 367  
 QY 361 CTGTCTGGGCTTCAGGCAACCGATGACGAGTCTGCGGCGGCGGAGCGGATTTGCAAT 420

DB 368 CTGTCTGGGCTTCAGGCAACCGGATGACGAGTCTGCGGTCGAGACCCCGATTGGCAT 427  
 QY 421 GTCAACAG-AAAAAGCTCGCTGACCTGCGCATTTGGCTTGGAGCAACGATNANGTG 479  
 DB 428 GTCAACAGAAAAAGCTCGCTGACCTGCGCATTTGGCTTGGAGCAACGATNANGTG 487  
 QY 480 CCGGAGCGGGAATTTGTTGTTGAGACAGACTCCGGGAGACMATGATCCCGTGAATCT 539  
 DB 488 CCGGAGCGGAG-ANTTGTGCTGTTGAGACAGACTCCGGGAGAGATGATCCCGTGAATCT 546  
 QY 540 CCGCGGAGCACTTAATATACCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 599  
 DB 547 GCGCGGAGCACTTAATATACCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 602  
 QY 600 TAAACNCAANTGGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 659  
 DB 603 TAAACNCAANTGGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660  
 QY 660 TCGATGAGACNCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 719  
 DB 661 TCGATGAGACCGG--TGTACAGTCCACATTTGCAATGCGGCTGCTGCTGCTGCTGCT 717  
 QY 720 NTGCCCAACNCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 777  
 DB 718 ATCACCAACNCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 777  
 QY 778 NGTCCCGCTGCTGCT 792  
 DB 778 TGTTCCTCTCTGATCACAATCTTTGCTCTGGAACCTGAGAGTGAAGAGGCG 792  
 RESULT 5  
 AAV69460 standard; cDNA; 727 BP.  
 ID AAV69460;  
 AC 15-MAR-1999 (first entry)  
 DT XX  
 DE Banana fruit ripening-related clone U-139 cDNA.  
 KW Fruit ripening; banana; modulator; tissue senescence; crop; plant;  
 KM triploid; plant breeding; ss.  
 OS Musa acuminata.  
 XX W09853085-A1.  
 PN 26-NOV-1998.  
 PD 05-MAY-1998; 98MO-GB01297.  
 PF 20-MAY-1997; 97GB-0010370.  
 PR (ZENNE ) ZENNECA LTD.  
 PA Bird CR, Medina-Suarez RDJ, Seymour GB;  
 XX WPI; 1999-059745/05.  
 DR New method of modulating fruit ripening or tissue senescence  
 XX characteristics of Musa plants - by introducing DNA sequences,  
 PT useful in processes for modifying plant/fruit ripening  
 PT characteristics  
 XX Claim 1; Page 30-31; 78pp; English.  
 PS AAV69440-V69512 are cDNA sequences which are used in a method to  
 CC modulate the fruit ripening or tissue senescence characteristics of Musa  
 CC acuminate (banana) plants. The method provides a recombinant way of  
 CC modulating ripening/senescence characteristics of bananas, which are a  
 CC globally important crop. In particular, the method can modulate such  
 CC characteristics in the dessert banana, which due to its triploid nature

CC Is unaffected by conventional plant breeding techniques.

XX Sequence 727 BP; 144 A; 199 C; 202 G; 157 T; 25 other;

Query Match 71.0%; Score 572.2; DB 20; Length 727;  
Best Local Similarity 90.9%; Pred. No. 2.4e-160;  
Matches 653; Conservative 0; Mismatches 57; Indels 8; Gaps 5;

```
QY 1 TGTTCCTCCTCGATGACATCTTTTGTCTGGGAAAGGTGAGAGTGAAGAGGGG 60
DB 16 TGTTCCTCCTCGATGACATCTTTTGTCTGGGAAAGGTGAGAGTGAAGAGGGG 75
QY 61 GCAATGACGGCGGGTTAAGATGATCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120
DB 76 GCAATGACGGCGGGTTAAGATGATCTCTCTCTCTCTCTCTCTCTCTCTCTCT 135
QY 121 CTGGTTTGAACGAGGAGTGGGGGTGATTTGAGAGGAGAGTCTCTGGCTGAGAA 180
DB 136 CTGGTTTGAACGAGGAGTGGGGGTGATTTGAGAGGAGAGTCTCTGGCTGAGAA 195
QY 181 GGGGAGCATCGCGGAGGAGCTTGAGAGAGGCTCCGCGAAGCGGAGCGCGATGCT 240
DB 196 GGGGAGCATCGCGGAGGAGCTTGAGAGAGGCTCCGCGAAGCGGAGCGCGATGCT 255
QY 241 TCTTTGAAGAGAGGCGCTGTAAACCGGAGAGAGAGCGGAGTGCAGCAGCCGAGAG 300
DB 256 TCTTTGAAGAGAGGCGCTGTAAACCGGAGAGAGAGAGCGGAGTGCAGCAGCCGAGAG 315
QY 301 GTTCTCTGACGCTCTCTGATGACATTAATCAACAGCAGGCTGCGAGATCTTGGTTAT 360
DB 316 GTTCTCTGACGCTCTCTGATGACATTAATCAACAGCAGGCTGCGAGATCTTGGTTAT 375
QY 361 CTGTCTGGGGTTGAGGAAACCGGATGAGAGAGTGTGGGGTGGGA-CCGTGATTTGGGA 419
DB 376 CTGTCTGGGGTTGAGGAAACCGGATGAGAGAGTGTGGGGTGGGA-CCGTGATTTGGGA 435
QY 420 TGTCAACAGAAAAAAGCTGCTGACTGCGGCTATTTGGAGCGACGCAATATGCTG 479
DB 436 TGTCAACAGAAAAAAGCTGCTGACTGCGGCTATTTGGAGCGACGCAATATGCTG 495
QY 480 CCGGAGCGGGGAATTTGTTGTTGTGACAGACTCCGGGAGCAATGATCCCGTGAATCCT 539
DB 496 CCGGAGCGGGGAATTTGTTGTTGTGACAGACTCCGGGAGCAATGATCCCGTGAATCCT 554
QY 540 CCGCGGGAACCTTANATACCCGCTCNCNCAANGAATTTGCCCCCTGCGGATCCCTT 599
DB 555 CCGCGGGAACCTTANATACCCGCTCNCNCAANGAATTTGCCCCCTGCGGATCCCTT 610
QY 600 TAAACNCAANTGGAATCTCNCNCAANGAAGAACTCTTATGACAGCTTAAACNA 659
DB 611 TAAACNCAANTGGAATCTCNCNCAANGAAGAACTCTTATGACAGCTTAAACNA 669
QY 660 TCGATGACNCTGTCTCTGTCACATTTGCCAATGCGCGCTGCTCACCANCAAT 717
DB 670 TCGATGACNCTGTCTCTGTCACATTTGCCAATGCGCGCTGCTCACCANCAAT 726
```

RESULT 6  
AAV28658  
ID AAV28658 standard; cDNA; 727 BP.  
XX  
AC AAV28658;  
XX  
DT 29-JUL-1998 (first entry)  
DE Ripening banana pulp cDNA clone U-089 SEQ ID NO:16.  
XX  
XX Banana; ripening; pulp; Musa acuminata cv. Grand Nain; fruit;  
KM genetic control; tissue senescence; ss.  
XX  
OS Musa acuminata.  
XX  
PN WO9811228-A2.

```
XX 19-MAR-1998.  
PD  
XX  
PF 08-SEP-1997; 97MO-GB02424.  
PR 25-APR-1997; 97GB-0008366.  
PR 10-SEP-1996; 96GB-0018862.  
XX  
PA (ZENEC ) ZENECA LTD.  
XX  
PI Bird CR, Medina-Suarez RDJ, Seymour GB;  
PI  
PI WPI; 1998-207389/18.  
DR  
XX  
XX Modulation of ripening or tissue senescence in bananas - comprises  
PT use of DNA isolated from ripening banana pulp to produce genetically  
PT modified fruit  
XX  
XX Claim 1; Page 28; 72pp; English.  
XX  
CC The present sequence represents a cDNA clone isolated from ripening  
CC banana pulp. 57 clones were isolated and are given in AAV28643 to  
CC AAV28699. The cDNA clone sequences can be used in a method of modulating  
CC ripening or tissue senescence process in plants of the genus Musa. The  
CC method comprises: (a) inserting into the plant material at least 1 of the  
CC 57 sequences (as above); (b) regenerating the plant material; and (c)  
CC selecting from the transformed regenerants, plants with modulated  
CC ripening or tissue senescence characteristics. Also described in the  
CC present invention are: (1) plants, their progeny, seed and material  
CC obtained from the plants, produced by the above method; (2) a vector  
CC functional in plants comprising a promoter region which is operably in  
CC plant cells; a polynucleotide sequence as defined above; and a  
CC transcription termination sequence; and (3) a method of controlling  
CC plant pathogens comprising the application of anti pathogenic agent to  
CC plants of (1).  
XX  
SQ Sequence 727 BP; 145 A; 205 C; 196 G; 159 T; 22 other;  
QY  
Query Match 67.5%; Score 543.8; DB 19; Length 727;  
Best Local Similarity 86.8%; Pred. No. 7e-152;  
Matches 628; Conservative 0; Mismatches 91; Indels 6; Gaps 4;  
QY 2 GTTCTCTCCTTCATGACATCTTTTGTCTGGGAAACGTGAGAGTGAAGAGGCGG 61  
DB 8 GTTCTCTCCTTCATGACATCTTTTGTCTGGGAAACGTGAGAGTGAAGAGGCGG 67  
QY 62 CAATGACGGGCGGTTTAAGATGATTCCTCTCTCTCTCTCTCTCTCTCTCTCTCT 121  
DB 68 CAATGACGGGCGGTTTAAGATGATTCCTCTCTCTCTCTCTCTCTCTCTCTCTCT 127  
QY 122 TGTGTTTGAACGAGAGTGGGGGTGATTTGGAAGCAGAGTCTCTGGCTGAGAAATG 181  
DB 128 TGTGTTTGAACGAGAGTGGGGGTGATTTGGAAGCAGAGTCTCTGGCTGAGAAATG 187  
QY 182 GCGGACATCGCGGAGAGAGCTTGAGAGAGGCTCCGCGAAGCGGAGCGGAGCGGATCT 241  
DB 188 GCGGACATCGCGGAGAGAGCTTGAGAGAGGCTCCGCGAAGCGGAGCGGAGCGGATCT 247  
QY 242 CATTGGAAGAGAGGCTGTAAACCGGAGCAGAAAGCCGAGTGCAGAGCCCGAGAGG 301  
DB 248 CATTGGAAGAGAGGCTGTAAACCGGAGCAGAAAGCCGAGTGCAGAGCCCGAGAGG 307  
QY 302 TTGCTTTCGACGGTCTGATGACATTAATCAACAGCAGGCTGCGAGATCTTGGTTATC 361  
DB 308 TTGCTTTCGACGGTCTGATGACATTAATCAACAGCAGGCTGCGAGATCTTGGTTATC 367  
QY 362 TGTCTGCGGTTTTCGAGCAACCGGATGAGAGAGTGTGGGGTGGGAGCCGATTTGAGATG 421  
DB 368 TGTCTGCGGTTTTCGAGCAACCGGATGAGAGAGTGTGGGGTGGGAGCCGATTTGAGATG 427  
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Db 187 GCGGACATCCGCGAGAGCTTGAGAGGCTCCGCGAAGCGGACCGCGATGCTT 246  
QY 242 CCTTGGAGAGAGGGCTGTAAACCCGGGACAGAGCCGAGTGCAGACGCCGAGAGG 301  
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QY 302 TTGCTTGCAGAGCTCTGATGATCATATATCAACAGACGGCTCGAGATCTTGGTTATC 361  
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AC AAC36622:  
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DT 17-OCT-2000 (first entry)  
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XX Arabidopsis thaliana DNA fragment SEQ ID NO: 14477.  
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XX Hybridisation assay; genetic mapping; gene expression control;  
KM protein identification; signal transduction pathway;  
KM metabolic pathway; promoter; termination sequence; ss.  
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OS Arabidopsis thaliana.  
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XX 05-MAY-1998; 98MO-GE01297.  
XX 20-MAY-1997; 97GB-0010370.  
XX (ZENE) ZENECA LTD.  
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PI Bird CR, Medina-Suarez RDJ, Seymour GB;  
XX WPI; 1999-059745/05.  
DR  
XX New method of modulating fruit ripening or tissue senescence  
PT characteristics of Musa plants - by introducing DNA sequences,  
PT useful in processes for modifying plant/fruit ripening  
PT characteristics  
XX  
PS Claim 1; Page 24; 78pp; English.  
XX  
CC AAV69440-V69512 are cDNA sequences which are used in a method to  
CC modulate the fruit ripening or tissue senescence characteristics of Musa  
CC acuminate (banana) plants. The method provides a recombinant way of  
CC modulating ripening/senescence characteristics of bananas, which are a  
CC globally important crop. In particular, the method can modulate such  
CC characteristics in the desert banana, which due to its triploid nature  
CC is unaffected by conventional plant breeding techniques.  
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SQ Sequence 823 BP; 168 A; 266 C; 222 G; 150 T; 17 other;

Query Match 18.7% Score 151; DB 20; Length 823;  
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QY 387 CGACGACTGCGCGGTGCGACCCCTGATGTCATGTCACAGAAAAAGCTCGTACTG 446  
DB 197 CGACGACTGCGCGGTGCGACCCCTGATGTCATGTCACAGAAAAAGCTCGTACTG 256  
QY 447 CGCATGCTGCTTGGACGACGACCCNATANGTGGCCCGGAGGAAATTTGTTGTTGTA 506  
DB 257 CGCATGCTGCTTGGACGACGACCCNATANGTGGCCCGGAGGAAATTTGTTGTTGTA 315  
QY 507 CACACTCCGGGAGCAGNATGATCCCGTGAATCTCGCCCGGAGACCTTAATACCCGTC 566  
DB 316 CCGACAGTGGCGGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 374  
QY 567 NTCCAANGAAGTTGCCCTCTGCGATCCCTTTAAACNCAANTGGAATCTCNCCTA 626  
DB 375 ATCCAGAGGAGGACCGCGTGT---GGATCATCTTCAAGCGGACATGCTATC-CAGTTGA 430  
QY 627 NGGAAGACTCNTTATGACAGCTTTAANCAATGATGACACNCGTGTCTGTCACA 686  
DB 431 AGGAGAGGACTCATCATCACTCCACAAAGCATCGACGCGCGGCGGACGTCACA 490  
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XX AAC42069;  
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XX  
DT 17-OCT-2000 (first entry)

XX Arabidopsis thaliana DNA fragment SPQ ID NO: 34171.  
DE Hybridisation assay; genetic mapping; gene expression control;  
XX protein identification; signal transduction pathway;  
KW metabolic pathway; promoter; termination sequence; ss.  
XX Arabidopsis thaliana.  
OS  
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PD 06-SEP-2000.  
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PF 25-FEB-2000; 2000EP-0301439.  
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Query Match 18.5%; Score 148.8; DB 21; Length 1526;  
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 DB 203 GAACATGCACTTGAGATATCAGAGAGTAGTCTGCTCAACCGAATCAATCGACGAT 262  
 OY 334 AGCAGCGCTGCGAGATCTCTGTTATCTGCTGCGGTTGAGCAACCGATGACGAC 393  
 DB 263 AGCAGCAGCAGAGAGATAGATCTCTGCTCAACCGAATCAATCGACGAT 322  
 OY 394 TCGTGGCGGTGCGACCTTATGTCATGTCACAGAAAAAGCTCCCTGACTGCGGCAAT 453  
 DB 323 TGTGGCGTGTGATGAGATGCGCAATCCCGGCAAAACATCTACCAATTCGCGCAATC 382  
 OY 454 GCGTTGAGCAGCAACGCAATGAGCGCGGAGAGGAAATGTTGCTGTGACAGACTC 513  
 DB 383 GGGTTCGTCGCGACACCAATCGAGGCGGAGAC-GGTCTTACTAGTAGTAGTAGACCC 441  
 OY 514 CGGGGACNATGATCCCGGTGAATCTCGCCCGGGAACACTTANATACCCCGCTNCTCAAN 573  
 DB 442 AAACGACGATTAACCCGGTTAATCTTAACCGGGGAACTTACGTACGCAATTAATCAAG 501

QY 574 GAACTGCCCCCTCTGGGATCCCTTTAAACNCAANTGGAATCTCNCNANGAGA 633  
 Db 502 AA-----GACCATATGATGATGCTTTAAACGTGACATGATCAATAA - TTAAGAGAGA 556  
 QY 634 ACTGNTATGACAGCTTTAAACNATGATGACNCGTCTCTGCTCCATTTGCCAA 693  
 Db 557 ACTATGATGACAGCTTTAAACNATGATGACNCGTCTCTGCTCCATTTGCCAA 616  
 QY 694 TGGCGCTGCTGACCAACCAATTTCTCCCAACNCTCTCTCCNCTGCTCCCTCC 753  
 Db 617 TGGTGCATGATGACGATGATGATGATGATGATGATGATGATGATGATGAT 676  
 QY 754 CAAT 757  
 Db 677 TGAT 680  
 RESULT 13  
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 ID AAV69445 standard; cDNA: 749 BP.  
 AC AAV69445;  
 XX 15-MAR-1999 (first entry)  
 DE Banana fruit ripening-related clone U-11 cDNA.  
 KW Fruit ripening; banana; modulator; tissue senescence; crop; plant;  
 KM triploid; plant breeding; ss.  
 OS Musa acuminata.  
 PN WO9853085-A1.  
 PD 26-NOV-1998.  
 PF 05-MAY-1998; 98WO-GB01297.  
 PR 20-MAY-1997; 97GB-0010370.  
 PA (ZENECA LTD.  
 PI Bird CR, Medina-Suarez RDJ, Seymour GB;  
 DR WPI; 1999-059745/05.  
 PT New method of modulating fruit ripening or tissue senescence  
 PT characteristics of Musa plants - by introducing DNA sequences,  
 PT useful in processes for modifying plant/fruit ripening  
 PT characteristics  
 PS Claim 1; Page 21-22; 78pp: English.  
 CC AAV69440-V69512 are cDNA sequences which are used in a method to  
 CC modulate the fruit ripening or tissue senescence characteristics of Musa  
 CC acuminata (banana) plants. The method provides a recombinant way of  
 CC modulating ripening/senescence characteristics of bananas, which are a  
 CC globally important crop. In particular, the method can modulate such  
 CC characteristics in the desert banana, which due to its triploid nature  
 CC is unaffected by conventional plant breeding techniques.  
 CC  
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 Query Match 17.9%; Score 144.4; DB 20; Length 749;  
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 Matches 275; Conservative 0; Mismatches 147; Indels 8; Gaps 5;

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 QY 445 TGGCGCATGCTGCTTGGACGACGACGACGACGACGACGACGACGACGACGAC 504  
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 QY 505 GACGACGCTGCGGGGACGACGACGACGACGACGACGACGACGACGACGACGAC 564  
 Db 314 GACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 372  
 QY 565 TCTGTCACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 624  
 Db 373 TCAATC-----AGGAGGAGCGCTGCTGATCATCTTCAAGCGCGACATGCTACCTG 428  
 QY 625 NANGAGAA-CCTGATGACGACGACGACGACGACGACGACGACGACGACGACGAC 683  
 Db 429 AAGAGGAGGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 488  
 QY 684 ACATGCGCAATGCGCGCTGCTGACGACGACGACGACGACGACGACGACGACGAC 743  
 Db 489 ACATCTCG 547  
 QY 744 CTCGCTGCTCC 753  
 Db 548 GTCCACATCC 557  
 RESULT 14  
 AAV28659  
 ID AAV28659 standard; cDNA: 842 BP.  
 AC AAV28659;  
 XX 29-JUL-1998 (first entry)  
 DE Ripening banana pulp cDNA clone U-U115 SEQ ID NO:17.  
 KW Banana; ripening; pulp; Musa acuminata cv. Grand Nain; fruit;  
 KM genetic control; tissue senescence; ss.  
 OS Musa acuminata.  
 PN WO9811228-A2.  
 PD 19-MAR-1998.  
 PF 08-SEP-1997; 97WO-GB02424.  
 PR 25-APR-1997; 97GB-0008366.  
 PR 10-SEP-1996; 96GB-0018862.  
 PA (ZENECA LTD.  
 PI Bird CR, Medina-Suarez RDJ, Seymour GB;  
 DR WPI; 1998-207389/18.  
 PT Modulation of ripening or tissue senescence in bananas - comprises  
 PT use of DNA isolated from ripening banana pulp to produce genetically  
 PT modified fruit  
 PS Claim 1; Page 28-29; 72pp: English.  
 CC The present sequence represents a cDNA clone isolated from ripening  
 CC banana pulp. 57 clones were isolated and are given in AAV28643 to  
 CC AAV28659. The cDNA clone sequences can be used in a method of modulating  
 CC ripening or tissue senescence processes in plants of the genus Musa. The  
 CC method comprises: (a) inserting into the plant material at least 1 of the  
 CC 57 sequences (as above); (b) regenerating the plant material, and (c)  
 CC selecting from the transformed regenerants, plants with modulated  
 CC ripening or tissue senescence characteristics. Also described in the  
 CC present invention are: (1) plants, their progeny, seed and material

CC obtained from the plants, produced by the above method; (2) a vector  
 CC functional in plants comprising a promoter region which is operably in  
 CC plant cells, a polynucleotide sequence as defined above, and a  
 CC transcription termination sequence; and (3) a method of controlling  
 CC plant pathogens comprising the application of anti-pathogenic agent to  
 CC plants of (1).

XX Sequence 842 BP; 177 A; 277 C; 218 G; 154 T; 16 other;

Query Match 17.7%; Score 142.8; DB 19; Length 842;  
 Best Local Similarity 64.3%; Pred. No. 3e-32;  
 Matches 276; Conservative 0; Mismatches 144; Indels 9; Gaps 5;

QY 325 ATAAATCAACAGCAGCGCTCGAGATCTTGTGTTATCTGTCGCGGTTCAAGCAACCG 384  
 DB 140 AGAAGCTTGAACGCTGTCCGGCGGCGACTGGGCTTCTGTATGGGCAACCGCAATCCG 199  
 QY 385 ATCGACGACTGCTGGCGGTGCGACCTGATGGCATGTCAACAGAAAAAGCTGCTGAC 444  
 DB 200 ATCGACGACTGCTGGCGGTGCGACCTGATGGCATGTCAACAGCGGCGCTGCTGAC 259  
 QY 445 TCGCGCATTTGCTTTGGACGCAAGCNAATANGTGGCCGCGACGGGAATTTGTCGTTGT 504  
 DB 260 TGGCCCATCGGGTTGCGGAAGACGCGATTTGGGGCAGGAGCGCG -AGATATACGTGT 318  
 QY 505 GACAGACTCCGGGACNATGATCCCGGATCCCGCGCGGGAACCTTANATACCGCG 564  
 DB 319 GACGACGACTGCTGGCGGTGCGACCTGATGGCATGTCAACAGCGGCGCTGCTGAC 377  
 QY 565 TCNTCCAAAGAGTTGCCCTCTGGGATCCCTTTAAACNCAANTGAAATCTCNCCTC 624  
 DB 378 TCATCC---AGGAGGAGCCGCTGTGATCATCTTCAAGCGGACATGTGTCATCCAGCT- 432  
 QY 625 NANGAAGACTCMTTATGACACAGCTTTAANCAATGATGACNCGTGTCTGTCGA 684  
 DB 433 GAAGAGAGAGCTCATATGAACCTCCACAGACCATGACGCGGCGGCGCAGGTCGA 492  
 QY 685 CATTGCAATGCGCGCTGCTCANTCACCANCAATTTTCCCAACATCTTCTCCNTNGC 744  
 DB 493 CATCTCCGGCGGCGGCTGCTATCACCAC -AGTACGTACCAACATCATCCACGGCG 550  
 QY 745 TCCTCCTCC 753  
 DB 551 TCACATCC 559

RESULT 15

AAV69448 standard; cDNA: 708 BP.

AAV69448;

15-MAR-1999 (first entry)

Banana fruit ripening-related clone U-31 cDNA.

FW Fruit ripening; banana; modulator; tissue senescence; crop; plant;  
 KW triploid; plant breeding; ss.

XX Musa acuminata.

OS MO9853085-A1.

PN 26-NOV-1998.

XX 05-MAY-1998; 98WO-GB01297.

PR 20-MAY-1997; 97GB-0010370.

PA (ZENEC) ZENEC LTD.

PI Bird CR, Medina-Suarez RDI, Seymour GB;

DR WPI; 1999-059745/05.

XX New method of modulating fruit ripening or tissue senescence  
 PT characteristics of Musa plants - by introducing DNA sequences,  
 PT useful in processes for modifying plant/fruit ripening  
 PT characteristics

XX Claim 1; Page 23; 78pp; English.

CC AAV69440-v69512 are cDNA sequences which are used in a method to  
 CC modulate the fruit ripening or tissue senescence characteristics of Musa  
 CC acuminata (banana) plants. The method provides a recombinant way of  
 CC modulating ripening/senescence characteristics of bananas, which are a  
 CC globally important crop. In particular, the method can modulate such  
 CC characteristics in the desert banana, which due to its triploid nature  
 CC is unaffected by conventional plant breeding techniques.

XX Sequence 708 BP; 140 A; 225 C; 192 G; 134 T; 17 other;

Query Match 17.5%; Score 141.4; DB 20; Length 708;  
 Best Local Similarity 60.3%; Pred. No. 7.2e-32;  
 Matches 290; Conservative 0; Mismatches 182; Indels 9; Gaps 5;

QY 325 ATAAATCAACAGCAGCGCTCGAGATCTTGTGTTATCTGTCGCGGTTCAAGCAACCG 384  
 DB 137 AGAAGCTTGAACGCTGTCCGGCGGCGACTGGGCTTCTGTATGGGCAACCGCAATCCG 196  
 QY 385 ATCGACGACTGCTGGCGGTGCGACCTGATGGCATGTCAACAGAAAAAGCTGCTGAC 444  
 DB 197 ATCGACGACTGCTGGCGGTGCGACCTGATGGCATGTCAACAGCGGCGCTGCTGAC 256  
 QY 445 TCGCGCATTTGCTTTGGACGCAAGCNAATANGTGGCCGCGACGGGAATTTGTCGTTGT 504  
 DB 257 TGGCCCATCGGGTTGCGGAAGACGCGATTTGGGGCAGGAGCGCG -ANATATACGTGT 315  
 QY 505 GACAGACTCCGGGACNATGATCCCGGATCCCGCGGGAACCTTANATACCGCG 564  
 DB 316 GACGACGACTGCTGGCGGTGCGACCTGATGGCATGTCAACAGCGGCGCTGCTGAC 374  
 QY 565 TCNTCCAAAGAGTTGCCCTCTGGGATCCCTTTAAACNCAANTGAAATCTCNCCTC 624  
 DB 375 TCATCC---ANGAGGAGCCGCTGTGATCATCTTCAAGCGGACATGTGTCATCCANCTG 430  
 QY 625 NANGAAGACTCMTTATGACACAGCTTTAANCAATGATGACNCGTGTCTGTCGA 684  
 DB 431 AAGGAGAGAGCTCATATGAACCTCCACAGACCTCAACGCGGCGGCGCAGGTCGA 490  
 QY 685 CATTGCAATGCGCGCTGCTCANTCACCANCAATTTTCCCAACATCTTCTCCNTNGC 743  
 DB 491 CATCTCCGGCGGCGGCTGCTATCACCACATCTTCTTCCNCAACATCATCTCCACGGC 550  
 QY 744 CTCCTCNC-TTCCCAATGCAACCCCGGGAATTCCTGCTCCCTCCCTCTCTATG 801  
 DB 551 GTCCACATCCACAGCTGCAATTCACANGGCGGGAATCTCTGCTGCGCACATCCCATNG 610  
 QY 802 G 802  
 DB 611 G 611

Search completed: June 19, 2003, 12:46:56  
 Job time : 184 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 19, 2003, 11:40:35 ; Search time 1102 Seconds  
(without alignments)  
11845.338 Million cell updates/sec

Title: US-09-966-881-13

Perfect score: 806  
Sequence: 1 TGTCTCTCCTTCATCACA.....TCCCTCTCTCTATGATNG 806

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Listing first 45 summaries

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EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hlc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	185	23.0	501	9	A1770665
2	176	21.8	480	9	AJ469163
3	173.6	21.5	589	17	A2135244
4	170	21.1	595	14	BQ741525
5	169.2	21.0	462	17	BH874844
6	166	20.6	800	14	BQ999911

7	165	20.5	720	14	BQ870176	BQ870176	OGDF08.Y
8	164.4	20.1	784	17	A2916009	A2916009	Psrt_1.h1
9	162.4	20.1	685	14	BQ795866	BQ795866	EST_4804
10	150	18.6	632	13	B1953076	B1953076	HVS&EN001
11	149.4	18.5	679	10	AV822011	AV822011	AV822011
12	149.2	18.5	883	10	BE035831	BE035831	MO10G11.M
13	144.8	18.0	612	14	BQ148154	BQ148154	NF062C07F
14	143.8	17.8	420	14	BQ134100	BQ134100	san57c10.
15	141.2	17.5	518	14	BQ104182	BQ104182	fc2443.e
16	141	17.5	365	12	BF655654	BF655654	FM1_47.B1
17	140.2	17.4	634	10	AM223193	AM223193	EST300004
18	139.8	17.3	549	12	BG599600	BG599600	EST504495
19	138.8	17.2	781	10	AW398301	AW398301	EST298148
20	133.8	16.6	632	14	BQ148911	BQ148911	NF084D12F
21	130.4	16.2	541	10	AV527067	AV527067	AV527067
22	130.2	16.2	542	12	BG040772	BG040772	NX51_114_
23	130	16.1	629	10	AV827058	AV827058	AV827058
24	129.6	16.1	620	10	AV825500	AV825500	AV825500
25	126.6	15.7	539	10	AV527181	AV527181	AV527181
26	126.4	15.7	579	10	AV442702	AV442702	AV442702
27	126.4	15.7	727	14	BQ634030	BQ634030	NXRV063.H
28	125.8	15.6	362	10	AV420958	AV420958	AV420958
29	124.4	15.4	635	14	BQ700242	BQ700242	NXRV103_B
30	124.2	15.4	609	17	BH717800	BH717800	BOMEY30TF
31	123.6	15.3	515	14	BQ634633	BQ634633	NXRV071_D
32	122.4	15.2	672	12	B1924648	B1924648	EST544537
33	122.4	15.2	686	14	BQ401767	BQ401767	GA_E0004
34	122.4	15.2	876	12	BG441931	BG441931	GA_Ea001
35	121.4	15.1	764	17	BH583673	BH583673	BOHJ209TF
36	120.4	14.9	436	12	BG319625	BG319625	SDHB12.SO
37	120.2	14.9	786	17	BH647126	BH647126	BOMB52TF
38	119.4	14.8	605	12	BG045860	BG045860	sa007c02.
39	117.4	14.6	666	12	BG599297	BG599297	EST504197
40	117.4	14.6	773	14	BQ508106	BQ508106	EST615521
41	116	14.4	728	14	BQ699768	BQ699768	NXRV128_F
42	115.4	14.3	473	13	BM492945	BM492945	NXRV_032_
43	115	14.3	546	12	BF008833	BF008833	ss70a05.Y
44	114.8	14.2	644	10	AM683073	AM683073	NF007A12L
45	114	14.1	567	13	B1471247	B1471247	sa195B04.

## ALIGNMENTS

RESULT 1	A1770665	501 bp	mRNA	linear	EST 02-FEB-2000
LOCUS	A1770665				
DEFINITION	606055G03.x2 606 - Ear tissue cDNA library from Schmidt lab Zea				
KEYWORDS	mays cDNA, mRNA sequence.				
ACCESSION	A1770665.1	GI:5268701			
VERSION	A1770665.1				
KEYWORDS	EST.				
SOURCE	Zea mays				
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC				
REFERENCE	1 (bases 1 to 501)				
AUTHORS	Walbot,V.				
TITLE	Maize ESTs from various cDNA libraries sequenced at Stanford University				
JOURNAL	Unpublished (1999)				
COMMENT	Contact: Walbot V. Department of Biological Sciences Stanford University 855 California Ave, Palo Alto, CA 94304, USA Tel: 650 723 2227 Fax: 650 725 8221 Email: walbot@stanford.edu Plate: 606055 row: G column: 03. Location/Qualifiers 1..501 /organism="Zea mays"				

[illegible][illegible]

High quality sequence start: 21  
High quality sequence stop: 547.  
Location/Qualifiers  
1. 589

/organism="Oryza sativa"  
/strain="Japonica"  
/cultivar="Nipponbare"  
/db\_xref="taxon:4530"  
/clone="OSJNB0115A18r"  
/clone\_lib="CUCI Rice BAC Library (EcoRI)"  
/rissue\_type="leaf"  
/lab\_host="E. coli DH10B"

/note="Vector: pBACindigo; site\_1: EcoRI; site\_2: EcoRI; Rice is the most important food crop in the world. Half of the world population, especially those inhabiting highly populated areas of the humid tropics and subtropics, rely on rice as their primary source of carbohydrate. Monocotyledonous rice is a diploid plant (2n=24) with a haploid genome equivalent of 431 Mbp (Arumuganathan and Earle, 1991). The relatively small genome of rice, three times larger than that of Arabidopsis, makes it suitable for genomic studies. In order to facilitate positional cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library from Oryza sativa, Nipponbare variety using EcoRI as the cloning enzyme. The library contains 55,296 clones with an average insert size of 121 kb providing approximately 15 haploid genome equivalents. The deep coverage allows the isolation a particular sequence with a probability of 99.9%. Three high density filters, each containing 18,432 clones (doubly spotted), represent the whole library for colony screening and can be requested from the Clemson University BAC/EST Resource Center ([www.genome.clemson.edu](http://www.genome.clemson.edu))."

BASE COUNT 121 a 203 c 171 g 3 others  
ORIGIN

Query Match 21.5%; Score 173.6; DB 17; Length 589;

Best Local Similarity 68.1%; Pred. No. 2,7e-41;  
Matches 297; Conservative 0; Mismatches 131; Indels 8; Gaps 5;

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OY 314 TCCGTGATGACATTAATCAAGACAGCGCTCGAGATCTCTGTTATCTGTCGGGTT 373
DB 1 TCATGAGGTGATCGAGAACACAGCGGAGAGAGCTGCTGTCGGCGCA 60
OY 374 CAGGCAACCCGATGACGATGCTGCGGCGGAGCCATGTCGATGCAACAGAAA 433
DB 61 CCGGCAATCGATCGACGACTCTGGAGGTGACCCGGAGCTGGCAAGAAATCGCCAGC 120
OY 434 AGCTGCTGACTGCGGCAATGCTTGGACGACGACGATGATGATGATGATGATGAT 493
DB 121 GGCTGGCGGATCGGCGCATGGCTTGGCGGCAAGCCATCGCGCGCGGAGC -GGCAAG 179
OY 494 TTGTTGTTGTGACAGACTCGGAGGACATGATCCCGGATTCCTGCGCGGAGAACT 553
DB 180 ATCTAGTGTGTGACGAGCCGACGACGACGA -CGGAGTGAACCCCAAGAGGGGACGCT 238
OY 554 TANAATACCCCGTCNTCCANAGAGTGGCCCTCTGGGATCCCTTTAACMCNANTGG 613
DB 239 CCGGTACGCCGTATCTCC -GCGAGAGAGCCGCTGTGATCTCTCAAGCCCGAGATAG 294
OY 614 AATATCTCNCNTNANAGAGAACTCTTATGACAGCTTAAANACATGATGACACNCT 673
DB 295 TGATACAGCTC -AAGCAGAGAGCTGATCATGAACAGTTTAAACATGACGCGCTGGC 353
OY 674 GTCTGTGTCACATGCGCAATGGCGCTGCTGACCAACCAATTTCTTCCCAACNTCT 733
DB 354 GCCAAGTGTGACATGCGCAATGGCGCTGCTGACCAACCAATTTCTTCCCAACNTCT 733
OY 734 GTTCCTGTCGTCACATGCGCAATGGCGCTGCTGACCAACCAATTTCTTCCCAACNTCT 733
DB 413 CATTCATGGCTGAC 428

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RESULT 4  
LOCUS B0741525  
DEFINITION sag19ell.y1 Gm-c1045 Glycine max cDNA clone SOYBEAN CLONE ID: 5'  
similar to TR:024416 024416 PECTATE LYASE; ; mRNA sequence.

ACCESSION B0741525  
VERSION B0741525.1  
KEYWORDS GI:21888312  
SOURCE soybean  
ORGANISM Glycine max

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine;

1 (bases 1 to 595)  
Shoemaker,R., Kelm,P., Vodkin,L., Erpelting,J., Coryell,V., Khanna,A., Bolla,B., Matra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Thelsing,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.

Public Soybean EST Project  
Unpublished (1999)  
Contact: Shoemaker R/Public Soybean EST Project  
Public Soybean EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@wustl.edu

This clone is available through: ResGen, Invitrogen Corp, 2130 South Memorial Parkway Huntville, AL 35801 For further information call: (800)-533-4363 or contact: [cust@resgen.com](mailto:cust@resgen.com) web site: [www.resgen.com](http://www.resgen.com)

Seq primer: -40RP from gibco  
High quality sequence stop: 430.

FEATURES  
source

1. 595  
Location/Qualifiers

/organism="Glycine max"  
/db\_xref="taxon:3847"  
/clone="SOYBEAN CLONE ID: 5"  
/clone\_lib="Gm-c1045"  
/rissue\_type="Hypocotyl, 9-10 day old etiolated seedlings"  
/lab\_host="DH10B"  
/note="Vector: pBluescriptII SK-; Site\_1: EcoRI; Site\_2: XhoI; This cDNA library was constructed from mRNA isolated from etiolated hypocotyl tissue of 9-10 day old seedlings of the cultivar Williams 82. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) primer with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by digestion with EcoRI and XhoI. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (Gibco BRL). This library was constructed by Dr. Randy Shoemaker."

BASE COUNT 149 a 171 c 169 g 106 t  
ORIGIN

Query Match 21.1%; Score 170; DB 14; Length 595;

Best Local Similarity 63.7%; Pred. No. 3.3e-40;  
Matches 307; Conservative 0; Mismatches 168; Indels 7; Gaps 4;

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OY 236 ATGCTTCTTGAAGAGAGGCTGTAAACCCGGACAGACCCGAGTGAAGACCCG 295
DB 117 ATTGCGAATGGCAGAAAGGTGACGAGAGCTTTGAATGAACATGAGTGAATTCAG 176
OY 296 AGGAGTGTCTGACAGGCTCTGATGACCATATATCAACAGCAGCGCTGCAATCTTG 355
DB 177 AGGAAATTTCTTCATGTTGATGAGAGATACGAACTACACGCGCTGAGAAAGACCTGA 236
OY 356 GTTATCTGTCGTGCGGTTTACGCAACCCGATGACGACGATGCTGGGCGTCCAGCTGATT 415

```







RESULT	9
LOCUS	AZ916009 784 bp DNA linear GSS 15-MAR-2001
DEFINITION	PstI_1_h12-c-1_0 Maize PstI B73 Leaf Zea mays genomic, DNA sequence.
ACCESSION	AZ916009
VERSION	AZ916009.1 GI:13347280
KEYWORDS	GSS.
SOURCE	Zea mays.
ORGANISM	Zea mays.
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoidae; Andropogoneae; Zea.
AUTHORS	Missouri Maize Project--Maize Mapping Project.
TITLE	PstI Zea mays B73 PstI leaf tissue library
JOURNAL	Unpublished (2001)
COMMENT	Contact: Schroeder S Missouri Maize Project--Maize Mapping Project University of Missouri 209 Curtis Hall, Columbia, MO 65211, USA Tel: 573 882 8214 Fax: 573 884 7850 Email: sschroeder@celephais.agron.missouri.edu Class: shotgun
FEATURES	Location/Qualifiers
Source	1..784
	/organism="Zea mays"
	/cultivar="B73"
	/db_xref="taxon:4577"
	/clone_lib="Maize PstI B73 Leaf"
	/tissue_type="Leaf"
	/lab_host="DH5 alpha"
	/note="Organ: Leaf; Vector: pUC19; PstI digested B73 genomic sucrose gradient size fractionated fragment sizes of 0.5kb to 2kb ligated to pUC19 transformed in DH5 alpha"
BASE COUNT	190 a 202 c 210 g 182 t
ORIGIN	
Query Match	20.4%; Score 164.4; DB 17; Length 784;
Best Local Similarity	70.0%; Pred. No. 1.9e-38;
Matches	266; Conservative 0; Mismatches 107; Indels 7; Gaps 4;
OY	319 ATGACCATATCAACAGCAGCGCTTCGCAGATCTTGGTTATCTGTCTGTCGCTTCAGGC 378
Db	
OY	412 AGTGCCATCAAGAACAAGCACGCCCGCGAACAACCTGGGTACTGTCTGCGGACAGGC 471
Db	
OY	379 AACCGATCGACGACTGCTGGCGGGCGGACCCCTATTGSCATGTCAACAGAAAAAGCTC 438
Db	
OY	472 AACCAGATCGACGACTGCTGGCGGGCGGACCCCTATTGSCATGTCAACAGAAAAAGCTC 531
Db	
OY	439 GCTGACTGCGCATTTGGCTTTGGACGCAACGCNATANGTGGCCGCGAGCGGGAAATTTGTT 498
Db	
OY	532 GCCGACTGGGCAATCGGGTTGGCGCGCAAGCCATCGCGGGCCGCGAC -GCCAAGGTGTA 590
Db	
OY	499 CGTTGTGACAGACTCCGGGGAACNATGATCCCGTGATCTCTGCGCCCGGGAAACTTANAT 558
Db	
OY	591 CGTGGTGGAGACCCGAGCGACGAGAT -CCGTGAACCCCGCGAGGGACACCTTCGCG 649
Db	
OY	559 ACCCGCTNTCCANGAAGTTGCCCCCTCTGGATCCCTTTAAACNNANTNGGAATC 618
Db	
OY	650 ACGCCGCTATCC ---AGAGAGACCCCGTGTGATCATCTTCAAGCGGGACATGCTGTATC 705
Db	
OY	619 TCNCTCNANGAAGAACTNTTATGAACAGCTTTAAANCNATGATGAGCNCNGTTCCT 678
Db	
OY	706 ACGET -GAGGAGAGAGCTCATCATGMAACAGTTTCAAGACCATCGAGGGCGCGGCCCA 764
Db	
OY	679 CGTCCACATTTGCCAATGGCG 698
Db	
OY	765 CGTGCACATCGCCAAGCGCG 784
Db	

LOCUS	BO795866	685 bp	mRNA	linear	EST 30-JUL-2002
DEFINITION	EST 4804 Ripening Grape berries Lambda Zap II Library Vitis vinifera cDNA clone RT021D12 3', mRNA sequence.				
ACCESSION	BO795866				
KEYWORDS	BO795866.1 GI:22010832				
SOURCE	EST.				
ORGANISM	Vitis vinifera.				
REFERENCE	Vitis vinifera.				
AUTHORS	Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Vitaceae; Vitis.				
TITLE	1 (bases 1 to 685)				
JOURNAL	Abdal,P., Agasse,A., Ageorges,A., Aranasova,R., Barrieu,F., Couture,C., Dedalendamp,F., Delrot,S., Glissant,D., Grimplet,J., Hamdi,S., Romieu,C. and Terrier,N. Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages Unpublished (2002)				
COMMENT	Contact: Romieu C. Unité de Recherche des Produits de la Vigne Institut National de la Recherche Agronomique 2, place Viala, 34 060 Montpellier Cedex 01, France Tel: 00-33-(0)4-99-61-28-62 Fax: 00-33-(0)4-99-61-28-57 Email: romieu@enscm.inra.fr Seq primer: T7.				
FEATURES	Location/Qualifiers				
source	1..685				
	/organism="Vitis vinifera"				
	/cultivar="Shiraz"				
	/db_xref="taxon:29760"				
	/clone="RT021D12"				
	/clone_id="Ripening Grape berries Lambda Zap II library"				
	/dev_stage="ripening stage"				
	/note="Organ: Fruit; Vector: Lambda Zap II; Site:1: Eco RI ; Site:2: XhoI. Oriented library construction described in Generation of ESTs from grape Berry (skin, pulp or seeds) at various developmental stages by Terrier,N., Ageorges,A., Abdal,P., Romieu,C. in J. Plant Physiol. 158 (12): 1575-83 2001"				
BASE COUNT	171 a 166 c 180 g 168 t				
ORIGIN					
Query Match	20.1%; Score 162.4; DB 14; Length 685;				
Best Local Similarity	62.8%; Pred. No. 7.2e-38;				
Matches 297; Conservative	0; Mismatches 169; Indels 7; Gaps 4;				
QY	280 GCACTGCACACCCCGGAGAGGTGCTTCGACGGTCTCGATGACCATTAATCAACAGACG 339				
DB	206 GCACTTATATGACCCAGATGACGTGCTTCAATGGTGGACATGACCATTTGGAAACAGACA 265				
QY	340 GCTTCGACAGTCCTTGGTTATCTCTGCTGCGGTTCAAGCAACCCGATCGAGCTGTGG 399				
DB	266 GAGGAGGAAGAAATTAGGTATTATTTCTGTGTGGAACTGGTAATCCATTGATGATGCTGG 325				
QY	400 CGTGCACACCTGATTTGGATGTGATGATGATGATGATGATGATGATGATGATGATGAT 459				
DB	326 CGATGTGACCAACAATTTGGCAAAAGAACCGTAAAGCGCTTGGACACTCGGCATTTGGCTTT 385				
QY	460 GGAGCAACCGCMTATNTGCGCGGAGCGGAGGGAATTTTGTGTTGTGACAGTCACGTCGGGA 519				
DB	386 GGGGGAATCAATTTGAGGCGCTGA-TGGACGCTTATGTGTGCTACTGACCTGTGTGA 444				
QY	520 CNAATGATCCCGTGAATCTTCGCCCGGGAACACTTAATACCCGCTNTCCAAANGAAGTT 579				
DB	445 TGAATGAT-CCTGTCAACCCCAAGCTGTGCACTCTGGCCATGCTGTATCC----AGAT 499				
QY	580 GCCCCTCTGGGATCCCTTTAAACNCNMAATGGAATCTCNCNANGAAGAACTCNC 639				
DB	500 GCTCTCTCTGGAATTTGTTCAAGCGAGACATGGTGTATCAACAT-GAAGCAGAGGCTCAT 558				
QY	640 TATGACACGCTTTAAACNCNATTCATGTGACACNCNGTGTCTGTGCACATTTGCCAATGGCCG 699				

Db 559 CATGACAGCTTCACAAACATGATGGCGGTGACATGTCACATGCTAATGAGAG 618  
 QY 700 CCGCNCACACACACATTCNTCCCAACNTCTCTCTCCNTCCCTCCACCTCC 752  
 Db 619 ATGCATCACCGCTCCATTTGTCACGATGTATTAATTCATGTCTTCACATCC 671

RESULT 10  
 B1959076 632 bp mRNA linear EST 22-OCT-2001  
 LOCUS HVSME0018A17f Hordeum vulgare rachis EST library HVCDA0015  
 DEFINITION (normal) Hordeum vulgare cDNA clone HVSME0018A17f, mRNA sequence.  
 ACCESSION B1959076  
 VERSION B1959076.1 GI:16310331  
 KEYWORDS EST.  
 SOURCE Hordeum vulgare.  
 ORGANISM Hordeum vulgare.  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae  
 1 (bases 1 to 632)  
 Wing, R., Close, T. J., Kleinbols, A., Wise, R., Chin, A., Begum, D., Frisch, D., Atkins, M., Yu, Y., Henry, D., Palmer, M., Rambo, T., Simmons, J., Oates, R. and Main, D.  
 Development of a genetically and physically anchored EST resource for barley genomics: Morex rachis cDNA library  
 Unpublished (2001)  
 Contact: Wing RA  
 Clemson University Genomics Institute  
 Clemson University  
 100 Jordan Hall, Clemson, SC 29634, USA  
 Tel: 864 656 7288  
 Fax: 864 656 4293  
 Email: twing@clemson.edu  
 Total bp bases = 473  
 Seq primer: AATTACCTCACTAAGG  
 High quality sequence stop: 613.  
 Location/Qualifiers  
 1. 632  
 /organism="Hordeum vulgare"  
 /cultivar="Morex"  
 /db\_xref="taxon:4513"  
 /clone="HVSME0018A17f"  
 /clone\_lib="Hordeum vulgare rachis EST library HVCDA0015 (normal)"  
 /tissue\_type="rachis"  
 /lab\_host="TJC121"  
 /note="Vector: pBluescript SK(-); Site\_1: EcoRI; Site\_2: XhoI. Plants were grown at Washington State University, Pullman, WA in a greenhouse, the rachises were excised and frozen in liquid nitrogen (Kleinbols lab). In the TJ Close lab at the University of California, Riverside total RNA was prepared, poly(A) was purified, one primary unamplified cDNA library was made, and 1 million pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids (Chin). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis see <http://www.genome.clemson.edu/projects/barley>. To order this clone see <http://www.genome.clemson.edu/orders> Also see Close TJ, Wing R, Kleinbols A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (<http://wheat.pw.usda.gov/g9pages/bgn/31/cover.html>)  
 125 a 246 c 171 g 89 t 1 others

Query Match 18.6%; Score 150; DB 13; Length 632;  
 Best Local Similarity 67.2%; Pred. No. 4e-34;  
 Matches 254; Conservative 0; Mismatches 117; Indels 7; Gaps 4;

QY 376 GGCACCCGATCGACACTGCTGGCGTGGACCTGATGGCATGCAACAGAAAAAG 435  
 Db 11 GGGACCCCATGACGACACTGCTGGCGTGGACCTGATGGCATGCAACAGAAAAAG 70  
 QY 436 CTCGCTGACTGGCGCATTTGGCTTGGACGCAACGCAATANGTGGCCGCGGCAATTT 495  
 Db 71 CTCGCCGATCGCGCATCGCTTCCGGCCCAACGCCATCGCGCGCGCAC-GGCAAGAT 129  
 QY 496 GTTCGTTTGACAGACTCGGGGAGCATATCCCGTGAATCCCTGCCCGGGAACCTTA 555  
 Db 130 CTAGGTGTACCGACGAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 189  
 QY 556 NATACCCGCTCCTCAANGAAGTTGGCCCTGTGGATCCCTTAAACNCAANTGAA 615  
 Db 190 GCTAGCGCGTCATCC---AGGACGAGCGGCTGTGATCATCTTCAAGGCGGACATGTC 245  
 QY 616 ATCTCCTCANGAAGAACTCTTATGAAACAGCTTAAACNATGATGACNCTGT 675  
 Db 246 ATCACCCTC-AGCCAGAGACTCATCATGAACAGCTTCAAGACATGAGCGCGCGCC 304  
 QY 676 CCGTGTCCACATTTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 735  
 Db 305 CAACGTGACATCGCCACAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 363  
 QY 736 TCCNTGCTCTCCCTCCCTCC 753  
 Db 364 TCCAGGCGCTCCACATCC 381

RESULT 11  
 AV822011 679 bp mRNA linear EST 01-APR-2002  
 LOCUS AV822011  
 DEFINITION AV822011 RAF14 Arabidopsis thaliana cDNA clone RAF104-19-N09 5', mRNA sequence.  
 ACCESSION AV822011  
 VERSION AV822011.1 GI:19864043  
 KEYWORDS EST.  
 SOURCE thale cress.  
 ORGANISM Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eustosids II; Brassicales; Brassicaceae; Arabidopsis.  
 1 (bases 1 to 679)  
 Seki, M., Narusaka, M., Ishida, J., Kamiya, A., Satou, M., Nakajima, M., Oono, Y., Sakurai, T., Carninci, P., Kawai, J., Itoh, M., Ishii, Y., Arakawa, T., Shibata, K., Shimagawa, A., Muramatsu, M., Hayashizaki, Y. and Shinozaki, K.  
 Large scale analysis of Arabidopsis full-length cDNA (2002b)  
 Unpublished (2002)  
 Contact: Motoaki Seki  
 Plant Functional Genomics Research Group  
 RIKEN Genomic Sciences Center  
 3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan  
 Tel: 81-298-36-4359  
 Fax: 81-298-36-9060  
 Email: mseki@rc.riken.go.jp  
 An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al., 1998). This clone is in a modified pBluescript vector as a SstI/XhoI insert. Please visit our web site ([http://www.gsc.riken.go.jp/e/plant/index\\_e.html](http://www.gsc.riken.go.jp/e/plant/index_e.html)) for further details.  
 Location/Qualifiers  
 1. 679  
 /organism="Arabidopsis thaliana"  
 /db\_xref="taxon:3702"  
 /clone="RAF104-19-N09"  
 /clone\_lib="RAF14"  
 /dev\_stage="rosette plants"



BASE COUNT	176 a	107 c	158 g	171 f
ORIGIN				

Db 498 ATGTATCATTCATGGTCTTCATATTCATGAT 529

KEYWORDS	EST.
SOURCE	soybean.

181 CATCGGTGCGCGTGA-TGGCAAAATCTATGTGTGCTACTGACCCCAAGGATATATGA-CCCT 238







FEATURE:  
NAME/KEY: CDS  
LOCATION: 26..1126  
FEATURE:  
NAME/KEY: mat\_peptide  
LOCATION: 89..1126  
US-08-467-023-94

Query Match 6.9%; Score 55.6; DB 3; Length 1170;  
Best Local Similarity 62.5%; Pred. No. 2,7e-07;  
Matches 85; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

QY 360 TCTGTGCGGTTCAGGCAACCGATGACGACTGCTGGCGGTGACCCCTGATTGSCA 419  
DB 73 TGTATCTTGTACTCTGATATCCCATCGACAGCTGCTGGAGAGGATTCGAACCTGGGA 132  
QY 420 TGTCAACAGAAAAAGCTGCTGACCTGGCATTTGGCTTTGGACGCAACGCAATGATGG 479  
DB 133 TCAAAACAGATGAGCTCCGACAGCTGTGCTGTGGATTGGAACTCCACCATGGAGG 192

QY 480 CCGCAGCGGGAATT 495  
DB 193 CAAAGGAGGATTTT 208

RESULT 2  
US-08-467-023-1  
Sequence 1, Application US/08467023  
Patent No. 6090386

GENERAL INFORMATION:  
APPLICANT: Griffith, Irwin J.;  
APPLICANT: Pollock, Joanne;  
APPLICANT: Bond, Julian F.;  
APPLICANT: Garman, Richard D;  
APPLICANT: Kuo, Mei-Chang;  
APPLICANT: Yeung, Siu-mel H.;  
APPLICANT: Brauer, Andrew;  
APPLICANT: Exley, Mark A.;  
APPLICANT: Powers, Steven P.  
TITLE OF INVENTION: Allergenic Proteins And Peptides From  
NUMBER OF SEQUENCES: 261  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunologic Pharmaceutical Corporation, Inc.  
STREET: 610 Lincoln St  
CITY: Waltham  
STATE: MA  
COUNTRY: USA  
ZIP: 02154

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/467,023  
FILING DATE: June 6, 1995  
CLASSIFICATION: 424

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/350,225  
FILING DATE: December 6, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Jane E. Remillard

REGISTRATION NUMBER: 38,872  
REFERENCE/DOCKET NUMBER: 025.6 USD2 (IMI-028CPD2)

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 227-7400

TELEFAX: (617) 227-5941

INFORMATION FOR SEO ID NO: 1:  
SEQUENCE CHARACTERISTICS:

LENGTH: 1337 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single

TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
ORIGINAL SOURCE:  
ORGANISM: CRYPTOMERIA JAPONICA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 66..1187  
FEATURE:  
NAME/KEY: mat\_peptide  
LOCATION: 129..1187  
US-08-467-023-1

Query Match 6.8%; Score 55.2; DB 3; Length 1337;  
Best Local Similarity 51.7%; Pred. No. 3.8e-07;  
Matches 181; Conservative 0; Mismatches 159; Indels 10; Gaps 3;

QY 349 TCTCTGTTATCTGTGTGCGGTTCAGGCAACCCGATTCAGCAGCTCTGGCGGTGAC 408  
DB 102 TCTTTGTAATTTGGATCTCTTTCTGATTAATCCATTAACAGCTCTGGAGGAGAC 161

QY 409 CCTGATGGCATGTCACAGAAAAAGCTGCTGACTGCGGCATTTGGCTTTGGACGCAAC 468  
DB 162 TCAAACTGGGCCCCAAATAGATGAGCTGCAAGATTGTGAGTGGCTTCGGAAGCTCC 221

QY 469 GCNATANGTGGCGCGCAGCGGGAATTTGTTGTTGACAGACTCCGGGACNATGATCC 528  
DB 222 ACATGGGAGGCAAGGAGAGAG-ATCTTTATAGGTCACAGACTCAGATGACGA----CC 276

QY 529 CCGTAATCTCTCGCGCGGGAACACTTANATACCCGCTCCTCCTCCTCCTCCTCCT 588  
DB 277 CTGTGAATCCTGACACGGAACCTGCGCTATGAGAGACCCGAGATGAGCCCTGTGGA 336

QY 589 GGGATCCCTTAACNCNANATGANAATCNCNCTNANAGAAAGACTCMTTATGAAAC 648  
DB 337 TAATTTCACTGGGAATATGAAATTAAGCTCAAAATGCTATGTAC-----ATGCTGG 391

QY 649 CTTTANANATGATGAGACNCGTCTGCTGTCACATTCGCAATGCGC 698  
DB 392 GTATAGACTTTTGTATGTCGAGGGGAGCACAAGTTTATATTGGCAATGGCG 441

RESULT 3  
US-08-467-023-96  
Sequence 96, Application US/08467023  
Patent No. 6090386

GENERAL INFORMATION:  
APPLICANT: Griffith, Irwin J.;  
APPLICANT: Pollock, Joanne;  
APPLICANT: Bond, Julian F.;  
APPLICANT: Garman, Richard D;  
APPLICANT: Kuo, Mei-Chang;  
APPLICANT: Yeung, Siu-mel H.;  
APPLICANT: Brauer, Andrew;  
APPLICANT: Exley, Mark A.;  
APPLICANT: Powers, Steven P.  
TITLE OF INVENTION: Allergenic Proteins And Peptides From  
NUMBER OF SEQUENCES: 261  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunologic Pharmaceutical Corporation, Inc.  
STREET: 610 Lincoln St  
CITY: Waltham  
STATE: MA  
COUNTRY: USA  
ZIP: 02154

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/467,023  
FILING DATE: June 6, 1995

CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/350,225  
FILING DATE: December 6, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Jane E. Remillard  
REGISTRATION NUMBER: 38,872  
REFERENCE/DOCKET NUMBER: 025.6 USD2 (IMI-028CPD2)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 227-7400  
TELEFAX: (617) 227-5941  
INFORMATION FOR SEQ ID NO: 96:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1278 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 36..1145  
FEATURE: NAME/KEY: mat-peptide  
LOCATION: 99..1145  
US-08-467-023-96

Query Match 6.7%; Score 54; DB 3; Length 1278;  
Best Local Similarity 61.8%; Pred. No. 8.0e-07;  
Matches 84; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 360 TCTGTCGTCGGTTCAGCAACCCGATCGACGACTGTCGGCGGTGACCCCTGATTGGCA 419  
DB 83 TGTACTGTGTCCTGTGATTAATCCATAGACAGCTGCTGGAGAGAGATTCGAATGGGG 142  
QY 420 TGTCAACAGAAAAAGCTGCTGACTGCGGCGATTGCTTTGGACGCAACGNATANGTGG 479  
DB 143 TCAAAACAGAAATGAAGCTGCGAGATTGCGCTGTGGATTGGAACTCCACCATGGAGG 202  
QY 480 CCGCGAGCGGGAATTT 495  
DB 203 CAAMGAGGAGATTTT 218

RESULT 4  
US-08-290-448A-58  
Sequence 58, Application US/08290448A  
Patent No. 5676954  
GENERAL INFORMATION:  
APPLICANT: Rogers, Bruce  
APPLICANT: Klapper, David G.  
APPLICANT: Rainier, Thorunn  
APPLICANT: Kuo, Wei-chang  
TITLE OF INVENTION: Allergenic Proteins From Ragweed and Uses  
NUMBER OF SEQUENCES: 93  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 60 State Street, suite 510  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109-1875  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/290,448A  
FILING DATE: August 15, 1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/529,951  
FILING DATE: May 29, 1990  
APPLICATION NUMBER: US 07/325,365

FILING DATE: March 17, 1989  
ATTORNEY/AGENT INFORMATION:  
NAME: Amy E. Mandragoras  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: IMI-018CN  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 227-7400  
TELEFAX: (617) 227-5941  
INFORMATION FOR SEQ ID NO: 58:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1328 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..1328  
US-08-290-448A-58

Query Match 5.8%; Score 46.6; DB 1; Length 1328;  
Best Local Similarity 46.7%; Pred. No. 0.00016;  
Matches 156; Conservative 0; Mismatches 171; Indels 7; Gaps 1;

QY 365 CCGCGGTTTCAGCAACCCGATCGACGACTGCTGGCGGGTGGCAACCCTGATTCATGTCA 424  
DB 113 CATGTGACACACACACATTTATAGACAGTCTGGAGGTGCAAGCCGTTGGCGAATA 172  
QY 425 ACAGAAAAAGCTGCTGACCTGCGGCGATTGCTTTGGACGCAACGNATANGTGGCGCG 484  
DB 173 ACCGACAAACGTTAGCCGATGTCGCCAAGTTTGGCAAGGAAACCTACGGTGGAAAC 232  
QY 485 ACGGGGATTTTGTGTTGTGACAGACTCGGGGACNATGATCCCGTAAATCTCGCCC 544  
DB 233 ATGGTAT-----GTCTACAGGTCACACAGTGAAGAATGATGATGTTCAATCA 285  
QY 545 GGAACACTTANATACCCGTCNCCAAAGAAAGTTGCCCCCTGGGATCCCTTAAAC 604  
DB 286 AAGAAGGACACTCCGTTTCTGCTGCGCCAAACAGGCCCTTGATGATTTTAA 345  
QY 605 NCNANTGGAATCTCNCNTNANGAAGACTNNTTATGACAGCTTTAANATGAT 664  
DB 346 ACAATATGTCATTCATTTGAATCAAGAGCTTGTGTAACAGGACCAACACATCAT 405  
QY 665 GCACNCTGTCTCTGTCACATTTGCCAATGGCG 698  
DB 406 GCGCGAGGGGTGAAGTTAATCATCGTTAACGCCG 439

RESULT 5  
US-08-290-448A-58  
Sequence 58, Application US/08290448A  
Patent No. 5698204  
GENERAL INFORMATION:  
APPLICANT: Rogers, Bruce  
APPLICANT: Klapper, David G.  
APPLICANT: Rainier, Thorunn  
APPLICANT: Kuo, Wei-chang  
TITLE OF INVENTION: Allergenic Proteins From Ragweed and Uses  
NUMBER OF SEQUENCES: 93  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 60 State Street, suite 510  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109-1875  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/290,448A  
FILING DATE: August 15, 1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/529,951  
FILING DATE: May 29, 1990  
APPLICATION NUMBER: US 07/325,365  
FILING DATE: March 17, 1989  
ATTORNEY/AGENT INFORMATION:  
NAME: Amy E. Mandragouras  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: IMI-018CN  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)227-5941  
INFORMATION FOR SEQ ID NO: 58:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1328 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..1328  
US-08-290-448A-38

Query Match 5.8%; Score 46.6; DB 1; Length 1328;  
Best Local Similarity 46.7%; Pred. No. 0.00016;  
Matches 156; Conservative 0; Mismatches 171; Indels 7; Gaps 1;

QY 365 CGTGGCGTTGAGCAACCCGATGACGACTGCTGGCGGTGCGACCTGATGGCATGTCA 424  
DB 113 CATGTAGAGCACACATATATAGACAAGTGTGAGGTGCAAGCCGATGGCGCAATA 172  
QY 425 ACAGAAAAAGCTCGCTGACTGGCGCATTTGGACCAACGCNATNATGCGCGG 484  
DB 173 ACCGAAAGGTTAGCGGATGTGCCAAGTTTTCAGAAAGGAACTTACGTTGGAATC 232  
QY 485 ACAGGAAATTTGCTGTGACAGACTCGGGGACNATGATCCCGTGAATCCTGCGCC 544  
DB 233 ATGGTAT-----GTCTACAGGTCACAGATGAATATATATGTGCAATCCA 285  
QY 545 GGAACACTTANATACCCCGTCNTCCANAGAGTTGCCCTCTGGGATCCCTTTAAC 604  
DB 286 AAGAAGGACACACTCGGTTTGTCTGCTGCCCAAAAGGCCCTTGTGATCATTTTAA 345  
QY 605 NCNAAATGAAATCTCNCNANGAAGAACTNTATGAACGCTTTAANACNATCGAT 664  
DB 346 AGAAATATGATGATTTGATTAATCAAGAGCTTGTGTAACAGCAAGACCATTCAT 405  
QY 665 GGACNCGTGTCTCGTCCACATTTGCCAATGGCG 698  
DB 406 GGCCGAGGGGTGAAGTTAAATCATCTTAACGCCG 439

RESULT 6  
US-08-175-069A-58  
Sequence 58, Application US/08175069A  
Patent No. 5776761

GENERAL INFORMATION:  
APPLICANT: Rogers, Bruce  
APPLICANT: Klapper, David G.  
APPLICANT: Rafnar, Thorunn  
APPLICANT: Kuo, Mei-chang  
TITLE OF INVENTION: Allergenic Proteins From Ragweed and Uses  
NUMBER OF SEQUENCES: 93  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD, LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109-1875

COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/175,069A  
FILING DATE: December 29, 1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/529,951  
FILING DATE: May 29, 1990  
APPLICATION NUMBER: US 07/325,365  
FILING DATE: March 17, 1989  
ATTORNEY/AGENT INFORMATION:  
NAME: Amy E. Mandragouras  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: IMI-018BV  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)227-5941  
INFORMATION FOR SEQ ID NO: 58:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1328 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..1328  
US-08-175-069A-58

Query Match 5.8%; Score 46.6; DB 1; Length 1328;  
Best Local Similarity 46.7%; Pred. No. 0.00016;  
Matches 156; Conservative 0; Mismatches 171; Indels 7; Gaps 1;

QY 365 CGTGGCGTTGAGCAACCCGATGACGACTGCTGGCGGTGCGACCTGATGGCATGTCA 424  
DB 113 CATGTAGAGCACACATATATAGACAAGTGTGAGGTGCAAGCCGATGGCGCAATA 172  
QY 425 ACAGAAAAAGCTCGCTGACTGGCGCATTTGGACCAACGCNATNATGCGCGG 484  
DB 173 ACCGAAAGGTTAGCGGATGTGCCAAGTTTTCAGAAAGGAACTTACGTTGGAATC 232  
QY 485 ACAGGAAATTTGCTGTGACAGACTCGGGGACNATGATCCCGTGAATCCTGCGCC 544  
DB 233 ATGGTAT-----GTCTACAGGTCACAGATGAATATATATGTGCAATCCA 285  
QY 545 GGAACACTTANATACCCCGTCNTCCANAGAGTTGCCCTCTGGGATCCCTTTAAC 604  
DB 286 AAGAAGGACACACTCGGTTTGTCTGCTGCCCAAAAGGCCCTTGTGATCATTTTAA 345  
QY 605 NCNAAATGAAATCTCNCNANGAAGAACTNTATGAACGCTTTAANACNATCGAT 664  
DB 346 AGAAATATGATGATTTGATTAATCAAGAGCTTGTGTAACAGCAAGACCATTCAT 405  
QY 665 GGACNCGTGTCTCGTCCACATTTGCCAATGGCG 698  
DB 406 GGCCGAGGGGTGAAGTTAAATCATCTTAACGCCG 439

RESULT 7

US-08-461-939B-58  
Sequence 58, Application US/08461939B  
Patent No. 6335019

GENERAL INFORMATION:  
APPLICANT: Rogers, Bruce  
APPLICANT: Klapper, David G.  
APPLICANT: Rafnar, Thorunn  
APPLICANT: Kuo, Mei-chang  
TITLE OF INVENTION: Methods For Treating Sensitivity To A  
TITLE OF INVENTION: Protein Allergen Using Peptides Which Include A T Cell Epit  
NUMBER OF SEQUENCES: 93

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,939B
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/464,000
FILING DATE: 05-JUN-1995
APPLICATION NUMBER: US 08/290,448
FILING DATE: 15-AUG-1994
APPLICATION NUMBER: US 07/529,951
FILING DATE: 29-MAY-1990
APPLICATION NUMBER: US 07/325,365
FILING DATE: 17-MAR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: INI-018CNDV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 1328 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1328
US-08-461-939B-58

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[illegible]

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US-08-464-000-58
; Sequence 58, Application US/08464000
; Patent No. 6335020
; GENERAL INFORMATION:
; APPLICANT: Rogers, Bruce
; APPLICANT: Klapper, David G.
; APPLICANT: Rafnar, Thorunn
; APPLICANT: Kuo, Mei-Chang
; TITLE OF INVENTION: Allergenic Peptides from Ragweed Pollen
; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IAHIVE & COCKFIELD, LLP
; STREET: 60 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,000
; FILING DATE: 05-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/290,448
; FILING DATE: 15-AUG-1994
; APPLICATION NUMBER: US 07/529,951
; FILING DATE: 29-MAY-1990
; APPLICATION NUMBER: US 07/325,365
; FILING DATE: 17-MAR-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Amy E. Mandragouras
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: IMI-018CN2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1328 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1328
; US-08-464-000-58

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[illegible]

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QY 665 GGACNCNGTCTCCTCGTCACATTTGCCAATGGCG 698  
Db 406 GGCCGAGGGGTGAAGTTAACTGCTTAACGCCG 439

## RESULT 9

US-08-290-448A-73  
Sequence 73, Application US/08290448A  
Patent No. 5676954  
GENERAL INFORMATION:

APPLICANT: Rogers, Bruce  
APPLICANT: Klapper, David G.  
APPLICANT: Rafnar, Thorunn  
APPLICANT: Kuo, Mei-chang  
TITLE OF INVENTION: Allergenic Proteins From Ragweed and Uses  
NUMBER OF SEQUENCES: 93  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 60 State Street, suite 510  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109-1875

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/290,448A  
FILING DATE: August 15, 1994  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/529,951  
FILING DATE: May 29, 1990  
APPLICATION NUMBER: US 07/325,365  
FILING DATE: March 17, 1989  
ATTORNEY/AGENT INFORMATION:  
NAME: Amy E. Mandragouras  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: IMI-018CN  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)227-5941

## INFORMATION FOR SEQ ID NO: 73:

## SEQUENCE CHARACTERISTICS:

LENGTH: 1349 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 1..1323

US-08-290-448A-73

Query Match 5.8%; Score 46.6; DB 1; Length 1349;

Best Local Similarity 46.7%; Pred. No. 0.00016;

Matches 156; Conservative 0; Mismatches 171; Indels 7; Gaps 1;

QY 365 CGTGGCTTCAGCAACCCGATGACGACTGCGGCGTGCGACCCCTGATTTGGCAGTCA 424

Db 134 CATGTAGAGACACACATATATAGACAGTGTGAGGTGCAAAAGCCGATTTGGCGAATA 193

QY 425 ACAGAAAAAGCTCGCTGACTGCGGCAATTGGCTTTGAGCCCAACGCNATANGTGGCCGC 484

Db 194 ACCGAAAGCGTATGCGGATTTGCCAAGGTTTCCAAAGGGAACCTACGCTGAAGAAAC 253

QY 485 ACGGGAATTTGCTTTGTGACAGACTCGGGGACNATGATCCCGTGAATCTGGCCC 544

Db 254 ATGGTAT-----GTCTACAGGTCACCACTGATTAAGATGATGATGTTGCAATCCA 306

QY 545 GGAACACTTANATACCCCGTCNTCCANAGAAGTTGCCCTCTGGATCCCTTTAAAC 604  
Db 307 AAAGAAAGCACACTCCGTTTGTCTGCCCCAAACAGCCCTTGTGATCATTTTAAA 366  
QY 605 NCNANTGGAATCTCNCCTCNANGAAGACTCTTTGAAACGCTTTAANACATGAT 664  
Db 367 AGAATATGCTGATTTGATTCAGATCAAGACTTGTCTTAACAGCAGCAAGACCATCGAT 426

## RESULT 10

US-08-290-448A-73  
Sequence 73, Application US/08290448A  
Patent No. 5698204  
GENERAL INFORMATION:

APPLICANT: Rogers, Bruce  
APPLICANT: Klapper, David G.  
APPLICANT: Rafnar, Thorunn  
APPLICANT: Kuo, Mei-chang  
TITLE OF INVENTION: Allergenic Proteins From Ragweed and Uses  
NUMBER OF SEQUENCES: 93  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 60 State Street, suite 510  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109-1875

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/290,448A  
FILING DATE: August 15, 1994  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/529,951  
FILING DATE: May 29, 1990  
APPLICATION NUMBER: US 07/325,365  
FILING DATE: March 17, 1989  
ATTORNEY/AGENT INFORMATION:  
NAME: Amy E. Mandragouras  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: IMI-018CN  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)227-5941

## INFORMATION FOR SEQ ID NO: 73:

## SEQUENCE CHARACTERISTICS:

LENGTH: 1349 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 1..1323

US-08-290-448A-73

Query Match 5.8%; Score 46.6; DB 1; Length 1349;

Best Local Similarity 46.7%; Pred. No. 0.00016;

Matches 156; Conservative 0; Mismatches 171; Indels 7; Gaps 1;

QY 365 CGTGGCTTCAGCAACCCGATGACGACTGCGGCGTGCGACCCCTGATTTGGCAGTCA 424

Db 134 CATGTAGAGACACACATATATAGACAGTGTGAGGTGCAAAAGCCGATTTGGCGAATA 193

QY 425 ACAGAAAAAGCTCGCTGACTGCGGCAATTGGCTTTGAGCCCAACGCNATANGTGGCCGC 484

Db 254 ATGGTAT-----GTCTACAGGTCACCACTGATTAAGATGATGATGTTGCAATCCA 306

DB 194 ACCGCAAGCGTTACCCGATTTGTGCCAAGGTTTTCGCAAGGGAACCTACGGTGGAAAC 253  
QY 485 ACGGGAAATTTGCTGTGTGACAGACTCCGGGACNMTGATCCCCGTAATCCTCGCC 544  
DB 254 ATGGGAT-----GTCTACACGGTCAACAGCTGATAAGATGATGATGTTGCAATCA 306  
QY 545 GGGAACTTANATACCCGTCNTCCANGAAGTTGCCCTTGGAATCCCTTTAAAC 604  
DB 367 AAGAAGGACACACTCGGTTTCTGCTGCCCCAAAAGAGCCCTTGATCTATTTTAA 366  
QY 605 NCNANTGGAATCTCNCNTCNANGAAGAACTNTATGACAGCTTTAANCAATCGAT 664  
DB 367 AGAATATGATGATTCATTGTAATCAAGAGCTTGCTGTAACAGGACAGACCAATCGAT 426  
QY 665 GGACNCGTCTCTGCTCCACATTCGCAATGCG 698  
DB 427 GGCCGAGGGGTGAAGTTAAACATCGTTAACGCCG 460

## RESULT 11

US-08-175-069A-73  
Sequence 73, Application US/08175069A  
Patent No. 5776761

GENERAL INFORMATION:

APPLICANT: Rogers, Bruce  
APPLICANT: Klapper, David G.

APPLICANT: Rafnar, Thorunn

APPLICANT: Kuo, Mel-chang

TITLE OF INVENTION: Allergenic Proteins From Ragweed and Uses

NUMBER OF SEQUENCES: 93

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD, LLP

STREET: 60 State Street

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02109-1875

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/175\_069A

FILING DATE: December 29, 1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/529,951

FILING DATE: May 29, 1990

APPLICATION NUMBER: US 07/325,365

FILING DATE: March 17, 1989

ATTORNEY/AGENT INFORMATION:

NAME: Amy E. Mandragouras

REGISTRATION NUMBER: 36,207

REFERENCE/DOCKET NUMBER: IM1-018DV

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617)227-7400

TELEFAX: (617)227-5941

INFORMATION FOR SEQ ID NO: 73:

SEQUENCE CHARACTERISTICS:

LENGTH: 1349 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 1..1323

US-08-175-069A-73

QY 365 CTGTGGCTTACGCAACCGATGACAGACTGCTGGCGGTCGACCCCTGATTTGCATGTCA 424  
DB 134 CATGTGAGACACACACATTTATGACAACTGCTGGAGGTGCAAAAGCCGATTTGGCGAATA 193  
QY 425 ACAGAAAAAGCTGCTGACCTGCGCATTTGCTTGGACGCAACGCMATANTGTCGCCG 484  
DB 194 ACCGCAAGCGTTAGCCGATTTGTCGCAAGGTTTTCGCAAGGGAACCTACGGTGGAAAC 253  
QY 485 ACGGGAAATTTGCTGTGTGACAGACTCCGGGACNMTGATCCCCGTAATCCTCGCC 544  
DB 254 ATGGGAT-----GTCTACACGGTCAACAGCTGATAAGATGATGATGTTGCAATCA 306  
QY 545 GGGAACTTANATACCCGTCNTCCANGAAGTTGCCCTTGGAATCCCTTTAAAC 604  
DB 307 AAGAAGGACACACTCGGTTTCTGCTGCCCCAAAAGAGCCCTTGATCTATTTTAA 366  
QY 605 NCNANTGGAATCTCNCNTCNANGAAGAACTNTATGACAGCTTTAANCAATCGAT 664  
DB 367 AGAATATGATGATTCATTGTAATCAAGAGCTTGCTGTAACAGGACAGACCAATCGAT 426  
QY 665 GGACNCGTCTCTGCTCCACATTCGCAATGCG 698  
DB 427 GGCCGAGGGGTGAAGTTAAACATCGTTAACGCCG 460

## RESULT 12

US-08-461-939B-73  
Sequence 73, Application US/08461939B  
Patent No. 635019

GENERAL INFORMATION:

APPLICANT: Rogers, Bruce  
APPLICANT: Klapper, David G.

APPLICANT: Rafnar, Thorunn

APPLICANT: Kuo, Mel-chang

TITLE OF INVENTION: Methods For Treating Sensitivity To A

NUMBER OF SEQUENCES: 93

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD, LLP

STREET: 28 State Street

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02109-1875

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/461\_939B

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/464,000

FILING DATE: 05-JUN-1995

APPLICATION NUMBER: US 08/290,448

FILING DATE: 15-AUG-1994

APPLICATION NUMBER: US 07/529,951

FILING DATE: 29-MAY-1990

APPLICATION NUMBER: US 07/325,365

FILING DATE: 17-MAR-1989

ATTORNEY/AGENT INFORMATION:

NAME: Amy E. Mandragouras

REGISTRATION NUMBER: 36,207

REFERENCE/DOCKET NUMBER: IM1-018CDV

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617)227-7400

TELEFAX: (617)742-4214

INFORMATION FOR SEQ ID NO: 73:

SEQUENCE CHARACTERISTICS:

LENGTH: 1349 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

Query Match 5.8%; Score 46.6; DB 1; Length 1349;  
Best Local Similarity 46.7%; Pred. No. 0.00016;  
Matches 156; Conservative 0; Mismatches 171; Indels 7; Gaps 1;

TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..1323  
US-08-461-9398-73

Query Match 5.8%; Score 46.6; DB 4; Length 1349;  
Best Local Similarity 46.7%; Pred. No. 0.00016;  
Matches 156; Conservative 0; Mismatches 171; Indels 7; Gaps 1;

QY 365 CGTGGGTTTCAGCAACCCGATGACGACCTGCTGGCGGTGCGACCCCTGATTGGCATGTCA 424  
DB 134 CATGTGAAGCACACACATTATAGACAGTGTGAGAGTGTGCAAGCCGATTGGCGGATA 193  
QY 425 ACAGAAAAAGCTCGCTGACTGCGGCGATTGCTTTGGACCAACGCNATNATGGCGCG 484  
DB 194 ACCGACAGCGTTAGCCGATTGTGCCAAGTTTGGAAAGGAACTACGGTGGGAAAC 253  
QY 485 ACGGGGAATTTGTTCTGTGACAGACTCGGGGACNATGATCCCGTGAATCCTCGCC 544  
DB 254 ATGTGTAT-----GTCTACAGCGTCACAGTGAATAGATGATGATGTTGCAATCCA 306  
QY 545 GGAACACTTANNTACCCCTCCTCCANAGAGTGGCCCTCTGGGATCCCTTTAAC 604  
DB 307 AAGAAGGACACACTCGGTTTCTGCTGCCAAACAGCGCCCTGTGGATCATTTTAA 366  
QY 605 NCNANTGGAATCTCNCNANGAAGACTCCTTATGAACAGCTTTAANACNATGAT 664  
DB 367 AGAAATATGTGTATTTATTTGATCAAGAGCTTGTGTAAACAGCCAGCAACACATGAT 426  
QY 665 GGACNCGTGTCTCTCCACATTTGCCATGGCG 698  
DB 427 GGCCGAGGGGTGAAGTTAACATCGTTAACGCCG 460

RESULT 13  
US-08-464-000-73  
Sequence 73, Application US/08464000  
Patent No. 6335020

GENERAL INFORMATION:  
APPLICANT: Rogers, Bruce  
APPLICANT: Klapper, David G.  
APPLICANT: Rainat, Thorunn  
APPLICANT: Kuo, Mei-chang  
TITLE OF INVENTION: Allergenic Peptides from Ragweed Pollen  
NUMBER OF SEQUENCES: 93  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHYE & COCKFIELD, LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109-1875

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/464,000  
FILING DATE: 05-JUN-1995

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/290,448  
FILING DATE: 15-AUG-1994  
APPLICATION NUMBER: US 07/529,951  
FILING DATE: 29-MAY-1990  
APPLICATION NUMBER: US 07/325,365  
FILING DATE: 17-MAR-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: Amy E. Mandragouras  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: IMT-018CN2

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)227-5941  
INFORMATION FOR SEQ ID NO: 73:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1349 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA

NAME/KEY: CDS  
LOCATION: 1..1323  
US-08-464-000-73

Query Match 5.8%; Score 46.6; DB 4; Length 1349;  
Best Local Similarity 46.7%; Pred. No. 0.00016;  
Matches 156; Conservative 0; Mismatches 171; Indels 7; Gaps 1;

QY 365 CGTGGGTTTCAGCAACCCGATGACGACCTGCTGGCGGTGCGACCCCTGATTGGCATGTCA 424  
DB 134 CATGTGAAGCACACACATTATAGACAGTGTGAGAGTGTGCAAGCCGATTGGCGGATA 193  
QY 425 ACAGAAAAAGCTCGCTGACTGCGGCGATTGCTTTGGACGCAACGCNATNATGGCGCG 484  
DB 194 ACCGACAGCGTTAGCCGATTGTGCCAAGTTTGGAAAGGAACTACGGTGGGAAAC 253  
QY 485 ACGGGGAATTTGTTCTGTGACAGACTCGGGGACNATGATCCCGTGAATCCTCGCC 544  
DB 254 ATGTGTAT-----GTCTACAGCGTCACAGTGAATAGATGATGATGTTGCAATCCA 306  
QY 545 GGAACACTTANNTACCCCTCCTCCANAGAGTGGCCCTCTGGGATCCCTTTAAC 604  
DB 307 AAGAAGGACACACTCGGTTTCTGCTGCCAAACAGCGCCCTGTGGATCATTTTAA 366  
QY 605 NCNANTGGAATCTCNCNANGAAGACTCCTTATGAACAGCTTTAANACNATGAT 664  
DB 367 AGAAATATGTGTATTTATTTGATCAAGAGCTTGTGTAAACAGCCAGCAACACATGAT 426  
QY 665 GGACNCGTGTCTCTCCACATTTGCCATGGCG 698  
DB 427 GGCCGAGGGGTGAAGTTAACATCGTTAACGCCG 460

RESULT 14  
US-08-232-463-14  
Sequence 14, Application US/08232463  
Patent No. 5670367

GENERAL INFORMATION:  
APPLICANT: DORNER, F.  
APPLICANT: SCHEIFLINGER, F.  
APPLICANT: FALKNER, F. G.  
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS  
NUMBER OF SEQUENCES: 52  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 1800 Diagonal Road, Suite 500  
CITY: Alexandria  
STATE: VA  
COUNTRY: USA  
ZIP: 22313-0299

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/232,463  
FILING DATE:

CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/935,313  
FILING DATE:



Search completed: June 19, 2003, 13:35:16  
Job time : 56 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 19, 2003, 12:40:30 ; Search time 123 Seconds

(without alignments)  
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Title: US-09-966-881-13

Perfect score: 806

Sequence: 1 TGTCTCTCTCTCATGACA.....TCCCTCTCTCTATGATG 806

Scoring table: IDENTITY\_NUC

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Searched: 1042519 seqs, 733713590 residues

Total number of hits satisfying chosen parameters: 2085038

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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3	536	66.5	724	10	US-09-966-881-18
4	142.8	17.7	842	10	US-09-966-881-17
5	134.6	16.7	687	10	US-09-966-881-14
6	124.2	15.4	1116	9	US-09-938-842A-1004
7	110.4	13.7	1215	9	US-09-938-842A-58
8	93.4	11.6	460	10	US-09-770-444-439
9	93	11.5	479	10	US-09-924-035A-174
10	74.4	9.2	1629	9	US-09-938-842A-1766
11	68.4	8.5	277	10	US-09-923-876-4484
12	64.4	8.0	1185	9	US-09-938-842A-809
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14	43.6	5.4	741	10	US-09-966-881-15
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17	37.4	4.6	708	9	US-10-123-155-298
18	35.6	4.4	360	10	US-09-864-761-27334
19	35.6	4.4	496	10	US-09-864-761-10689

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23	34.8	4.3	451	9	US-10-123-155-126
24	34.4	4.3	1732	10	US-09-789-561-21
25	34.2	4.2	4100	9	US-09-373-658-29
26	34	4.2	2396	9	US-10-098-841-96
27	34	4.2	2663	9	US-10-098-841-97
28	34	4.2	4332	9	US-09-764-891-5756
29	34	4.2	7149	9	US-10-196-935A-1
30	34	4.2	14155	9	US-10-108-603-102
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35	33.4	4.1	671	9	US-10-184-634-346
36	33.4	4.1	2380	9	US-09-964-992A-4
37	33.2	4.1	407	10	US-09-878-574-4048
38	33	4.1	519	9	US-10-123-155-210
39	32.8	4.1	638	9	US-10-150-762-1
40	32.8	4.1	661	9	US-10-121-988-34
41	32.8	4.1	661	10	US-09-894-998-34
42	32.8	4.1	1064	10	US-09-804-662-29
43	32.8	4.1	2481	9	US-10-121-988-35
44	32.8	4.1	2481	9	US-10-121-988-35
45	32.8	4.1	2481	10	US-09-894-998-35

#### ALIGNMENTS

RESULT 1

US-09-966-881-13

Sequence 13, Application US/09966881

Patent No. US20020120960A1

GENERAL INFORMATION:

APPLICANT: Seymour, Graham

Blid, Collin

Medina-Sanchez, Rosybel

TITLE OF INVENTION: Genetic control Of Fruit Ripening

NUMBER OF SEQUENCES: 57

CORRESPONDENCE ADDRESS:

ADDRESSER: Zeneca Ag Products Inc.

STREET: 1800 Concord Pike

CITY: Wilmington

STATE: DE

COUNTRY: USA

ZIP: 19850

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/966, 881

FILING DATE: 28-Sep-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/242, 860

FILING DATE: 29-Mar-1999

APPLICATION NUMBER: GB 9618862.8

FILING DATE: 10-Sep-1996

APPLICATION NUMBER: GB 9708366.1

FILING DATE: 25-Apr-1997

APPLICATION NUMBER: PCT/GB97/02424

FILING DATE: 08-Sep-1997

ATTORNEY/AGENT INFORMATION:

NAME: Hohenschultz, Liza D.

REGISTRATION NUMBER: 33,712

REFERENCE/DOCKET NUMBER: SEE 50183/UST

TELECOMMUNICATION INFORMATION:

TELEPHONE: (302) 886-1699

INFORMATION FOR SEQ ID NO: 13:





GENERAL INFORMATION:  
APPLICANT: Seymour, Graham  
Bird, Colin  
Medina-Suarez, Rosybel  
TITLE OF INVENTION: Genetic control of Fruit Ripening  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Zeneca Ag Products Inc.  
STREET: 1800 Concord Pike  
CITY: Wilmington  
STATE: DE  
COUNTRY: USA  
ZIP: 19850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/966,881  
FILING DATE: 28-Sep-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/242,860  
FILING DATE: 29-Mar-1999  
APPLICATION NUMBER: GB 9618862.8  
FILING DATE: 10-SEP-1996  
APPLICATION NUMBER: GB 9708366.1  
FILING DATE: 25-APR-1997  
APPLICATION NUMBER: PCT/GB97/02424  
FILING DATE: 08-SEP-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Hohenschutz, Liza D.  
REGISTRATION NUMBER: 33,712  
REFERENCE/DOCKET NUMBER: SEE 50183/UST  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (302) 886-1699  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 842 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONE: U-0115  
SEQUENCE DESCRIPTION: SEQ ID NO: 17:  
US-09-966-881-17

Query Match 17.7%; Score 142.8; DB 10; Length 842;  
Best local Similarity 64.3%; Pred. No. 1.9e-36;  
Matches 276; Conservative 0; Mismatches 144; Indels 9; Gaps 5;

325 ATATATACAGCAGCGCTGCGAGATCTCTTGGTTATCTGTGCGGCTTACAGCAACCG 384  
140 AGAAGCTTGAAGCTGTGCGGCGCGCGAGCTGCTTGTCTCATGCGGCAACCGCATCCG 199  
385 ATCGAGACTGCTGGGGTGGCGACCTGATTTGGCATGTCAACGAAAGAAAGCTCGGTGAC 444  
200 ATCGAGACTGCTGGGGTGGCGACCTGATTTGGCATGTCAACGAGGAGGCTCGGTGAC 259  
445 TCGCGATTGGCTTTGGACGCAACGCMATANGTGGCGCGAGCGGGGAATTTGCTTGTG 504  
260 TCGCGCATGGGTGGGGAAGAACGCGATTTGGGCGAGGAGCGCGC-AGATATAGCTGGT 318  
505 GACAGACTCGCGGAGCATGATCCCGTGAATCTTCCCGGAGACATTATATACCGCG 564  
319 GACCGCACTGGGAGACGA-CCCGGTATTCGAAACGGGCGACGCTCGGTACGCGC 377  
565 TCTTCCAAAGAGTTCCCGCTGCGATCCCTTAAACNCAANTGAATTCATCNCNC 624  
378 TCAATC---AGAGAGAGCGGCTGTGATCATCTTCAAGCGGACATGTGATCATCAGCT- 432

625 NANGAAGACTCCTTATGAACAGCTTTAANACNATGATGACNCGTCTCTGTCGA 684  
433 GAAGAGAGACTCATCATGATGAACCTCCACAGACCATGACGGCGGCGCCAGCGTCCA 492  
685 CATTCGCAATGGCGCTGCTTCACACNCAATTTCCCAACNTCTTTCCGNTGCC 744  
493 CATCTCGGGGGCGGCTGATCAACACC--AGTACGTACCAACATCATCATCAGCGCG 550  
745 TCCNCTGCC 753  
551 TCCCATCTCC 559

RESULT 5  
US-09-966-881-14  
Sequence 14, Application US/09966881  
Patent No. US20020120960A1  
GENERAL INFORMATION:  
APPLICANT: Seymour, Graham  
Bird, Colin  
Medina-Suarez, Rosybel  
TITLE OF INVENTION: Genetic control of Fruit Ripening  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Zeneca Ag Products Inc.  
STREET: 1800 Concord Pike  
CITY: Wilmington  
STATE: DE  
COUNTRY: USA  
ZIP: 19850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/966,881  
FILING DATE: 28-Sep-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/242,860  
FILING DATE: 29-Mar-1999  
APPLICATION NUMBER: GB 9618862.8  
FILING DATE: 10-SEP-1996  
APPLICATION NUMBER: GB 9708366.1  
FILING DATE: 25-APR-1997  
APPLICATION NUMBER: PCT/GB97/02424  
FILING DATE: 08-SEP-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Hohenschutz, Liza D.  
REGISTRATION NUMBER: 33,712  
REFERENCE/DOCKET NUMBER: SEE 50183/UST  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (302) 886-1699  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 687 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONE: U-069  
SEQUENCE DESCRIPTION: SEQ ID NO: 14:  
US-09-966-881-14

Query Match 16.7%; Score 134.6; DB 10; Length 687;  
Best local Similarity 61.6%; Pred. No. 8.5e-34;  
Matches 276; Conservative 0; Mismatches 163; Indels 9; Gaps 5;

325 ATATATACAGCAGCGCTGCGAGATCTCTTGGTTATCTGTGCGGCTTACAGCAACCG 384  
140 AGAAGCTTGAAGCTGTGCGGCGCGAGCTGCTTGTCTCATGCGGCAACCGCATCCG 199

OY 385 ATCGAGACTGCTGGCGGTGCGACCTGATGGCATGTCACAGAAAAAGCTCGTGAC 444  
|||||  
Db 200 ATCGAGACTGCTGGCGGTGCGACCTGATGGCATGTCACAGAAAAAGCTCGTGAC 259  
445 TCGCGCATGCTGGCGGTGCGACCTGATGGCATGTCACAGAAAAAGCTCGTGAC 504  
|||||  
Db 260 TCGCGCATGCTGGCGGTGCGACCTGATGGCATGTCACAGAAAAAGCTCGTGAC 318  
505 GACAGACTGCGGGGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 564  
|||||  
Db 319 GACCGACACTGCGGGGACGACGACGACGACGACGACGACGACGACGACGACGAC 377  
565 TCTCCAAAGAAAGTTGCGCGGTGCGACCTGATGGCATGTCACAGAAAAAGCTCGTGAC 624  
|||||  
Db 378 TCTCCAAAGAAAGTTGCGCGGTGCGACCTGATGGCATGTCACAGAAAAAGCTCGTGAC 434  
625 NANGAAGAAAGTTGCGCGGTGCGACCTGATGGCATGTCACAGAAAAAGCTCGTGAC 682  
|||||  
Db 435 AAGGAAGAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 494  
683 CACATGCGCAATGCGCGGTGCGACCTGATGGCATGTCACAGAAAAAGCTCGTGAC 742  
|||||  
Db 495 CACATGCGCAATGCGCGGTGCGACCTGATGGCATGTCACAGAAAAAGCTCGTGAC 552  
743 CCGTCGCAATGCGCGGTGCGACCTGATGGCATGTCACAGAAAAAGCTCGTGAC 770  
|||||  
Db 553 GCGTCGCAATGCGCGGTGCGACCTGATGGCATGTCACAGAAAAAGCTCGTGAC 580

## RESULT 6

US-09-938-842A-1004  
; Sequence 1004, Application US/09938842A  
; Patent No. US20020160378A1  
; GENERAL INFORMATION:  
; APPLICANT: Harper, Jeff  
; APPLICANT: Kreps, Joel  
; APPLICANT: Wang, Xun  
; APPLICANT: Zhu, Tong  
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING  
; FILE REFERENCE: SAME, AND METHODS OF USE  
; CURRENT FILING DATE: 2001-08-24  
; PRIOR FILING DATE: 2000-08-24  
; PRIOR APPLICATION NUMBER: US 60/227,866  
; PRIOR FILING DATE: 2000-08-24  
; PRIOR APPLICATION NUMBER: US 60/264,647  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/300,111  
; PRIOR FILING DATE: 2001-06-22  
; NUMBER OF SEQ ID NOS: 5379  
; SEQ ID NO 1004  
; LENGTH: 1116  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
US-09-938-842A-1004

Query Match 15.4%; Score 124.2; DB 9; Length 1116;  
Best Local Similarity 60.2%; Pred. No. 2.7e-30;  
Matches 241; Conservative 0; Mismatches 152; Indels 7; Gaps 3;

OY 319 AAGACATATATCAACAGCAGCGCTGCGACATCTCTGTTATCTGTCGCGGTGACGC 378  
|||||  
Db 1 AAGACATATATCAACAGCAGCGCTGCGACATCTCTGTTATCTGTCGCGGTGACGC 60  
379 AAGCCGATGAGAGCTGCTGGCGGTGCGACCTGATGGCATGTCACAGAAAAAGCTC 438  
|||||  
Db 61 AAGCCGATGAGAGCTGCTGGCGGTGCGACCTGATGGCATGTCACAGAAAAAGCTC 120  
439 GCTGACTGCGCATGCTGGCGGTGCGACCTGATGGCATGTCACAGAAAAAGCTC 498  
|||||  
Db 121 GCGGATGCGCATGCTGGCGGTGCGACCTGATGGCATGTCACAGAAAAAGCTC 179

OY 499 CGTTGACAGACTCGCGGGACGACGACGACGACGACGACGACGACGACGACGACGAC 558  
|||||  
Db 180 CGTTGACAGACTCGCGGGACGACGACGACGACGACGACGACGACGACGACGACGAC 238  
559 ACCCGCTGTCGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 618  
|||||  
Db 239 ACCCGCTGTCGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 293  
619 TCGCTGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 678  
|||||  
Db 294 TCGCTGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 353  
679 CGTTGACAGACTCGCGGGACGACGACGACGACGACGACGACGACGACGACGACGAC 718  
|||||  
Db 354 CGTTGACAGACTCGCGGGACGACGACGACGACGACGACGACGACGACGACGACGAC 393

## RESULT 7

US-09-938-842A-58  
; Sequence 58, Application US/09938842A  
; Patent No. US20020160378A1  
; GENERAL INFORMATION:  
; APPLICANT: Harper, Jeff  
; APPLICANT: Kreps, Joel  
; APPLICANT: Wang, Xun  
; APPLICANT: Zhu, Tong  
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING  
; FILE REFERENCE: SAME, AND METHODS OF USE  
; CURRENT FILING DATE: 2001-08-24  
; PRIOR FILING DATE: 2000-08-24  
; PRIOR APPLICATION NUMBER: US 60/227,866  
; PRIOR FILING DATE: 2000-08-24  
; PRIOR APPLICATION NUMBER: US 60/264,647  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/300,111  
; PRIOR FILING DATE: 2001-06-22  
; NUMBER OF SEQ ID NOS: 5379  
; SEQ ID NO 58  
; LENGTH: 1215  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
US-09-938-842A-58

Query Match 13.7%; Score 110.4; DB 9; Length 1215;  
Best Local Similarity 59.0%; Pred. No. 9.1e-26;  
Matches 239; Conservative 0; Mismatches 159; Indels 7; Gaps 4;

OY 353 TTGGTTATCTGCTGCGGTGCGACGACGACGACGACGACGACGACGACGACGACGACGAC 412  
|||||  
Db 147 TTGGTTATCTGCTGCGGTGCGACGACGACGACGACGACGACGACGACGACGACGACGAC 206  
413 ATTGCTATCTGCTGCGGTGCGACGACGACGACGACGACGACGACGACGACGACGACGAC 472  
|||||  
Db 207 ATTGCTATCTGCTGCGGTGCGACGACGACGACGACGACGACGACGACGACGACGACGAC 266  
473 TANGTGCGCGGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 532  
|||||  
Db 267 TANGTGCGCGGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 324  
533 GAATCTGCGCGGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 592  
|||||  
Db 325 GAATCTGCGCGGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 380  
593 TCGCTGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 652  
|||||  
Db 381 TCGCTGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 439  
653 AANACGATGATGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 712  
|||||  
Db 440 AANACGATGATGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 499  
713 CAATTCGTCGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 757







RESULT 13  
US-09-878-574-3663  
; Sequence 3663, Application US/09878574  
; Patent No. US20020110548A1  
; GENERAL INFORMATION:  
; APPLICANT: Byrum, Joseph R.  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Thompson, Michael D.  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
; TITLE OF INVENTION: Plants  
; FILE REFERENCE: 38-21(15401)B  
; CURRENT APPLICATION NUMBER: US/09/878,574  
; CURRENT FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: 09/333,535  
; PRIOR FILING DATE: 1999-06-14  
; NUMBER OF SEQ ID NOS: 15775  
; SEQ ID NO 3663  
; LENGTH: 388  
; TYPE: DNA  
; ORGANISM: glycine max  
; OTHER INFORMATION: Clone ID: LIB3028-007-Q1-B1-E8  
US-09-878-574-3663

Query Match 7.0%; Score 56.2; DB 10; Length 388;  
Best Local Similarity 52.5%; Pred. No. 3.2e-08;  
Matches 189; Conservative 0; Mismatches 164; Indels 7; Gaps 4;

QY 378 CAACCCGATGAGAGCTGCTGGGGGCGGAGCCCTGATGCTACAGCAAGAAAGCT 437  
Db 35 CAACCCGATGAGAGCTGCTGGGGGCGGAGCCCTGATGCTACAGCAAGAAAGCT 94  
QY 438 CGCTGATGCGGATGCTGCTGGGGGCGGAGCCCTGATGCTACAGCAAGAAAGCT 497  
Db 95 AGCAGAGTGGGGAAGAGGTGGGAAGAGCGGCCACCGGGGCTGCTGCCATCTA 154  
QY 498 TCGTGTGACAGACTCCGGGAGCAGATCCCGTGAATCTCCCGGGAACACTTANA 557  
Db 155 T-TCTGTACAGCAATTCGATGAGCA-CATGCTGAACCTTAAGCGGGAACACTTCCGT 212  
QY 558 TACCCTGCTCCAGAAAGTTGCCCTCTGGGATCCCTTAACNCNAATGGAAT 617  
Db 213 CAGCGTGTACCCAAAAGG---CCCTGTGATGATCTTGGACACAGCATGATCAT 268  
QY 618 CTCTCTCANGAAGACTCTTATTAACAGCTTTAANACATGATGAGCAGCTGCC 677  
Db 269 CAGTTT-GAGGCAAGAGCTGATGATTTCTCCGACAAGACATGATGCTGGGCA 327  
QY 678 TCGTCCACATGCGCAATGGCGCTGCTACACANCCATTTCTCCCAACNTCTTCT 737  
Db 328 ACCTGCAATTTAGGGGCGGTGCTGCTCACCATTCAGTTCTGAAACACGTTATATCC 387

## RESULT 14

US-09-966-881-15  
; Sequence 15, Application US/09966881  
; Patent No. US20020120960A1  
; GENERAL INFORMATION:  
; APPLICANT: Seymour, Graham

Medina-Suarez, Rosybel  
TITLE OF INVENTION: Genetic control of Fruit Ripening  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Zeneca Ag Products Inc.  
STREET: 1800 Concord Pike  
CITY: Wilmington  
STATE: DE  
COUNTRY: USA  
ZIP: 19850

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/966,881  
FILING DATE: 28-Sep-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/242,860  
FILING DATE: 29-Mar-1999  
APPLICATION NUMBER: GB 9618862.8  
FILING DATE: 10-SEP-1996  
APPLICATION NUMBER: GB 9708366.1  
FILING DATE: 25-APR-1997  
APPLICATION NUMBER: PCT/GB97/02424  
FILING DATE: 08-SEP-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Hohenschultz, Liza D.  
REGISTRATION NUMBER: 33,712  
REFERENCE/DOCKET NUMBER: SEE 50183/UST  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (302) 886-1699  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 741 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONE: U-084  
SEQUENCE DESCRIPTION: SEQ ID NO: 15:  
US-09-966-881-15

Query Match 5.4%; Score 43.6; DB 10; Length 741;  
Best Local Similarity 65.6%; Pred. No. 0.00056;  
Matches 84; Conservative 0; Mismatches 41; Indels 3; Gaps 2;

QY 681 TCCACATGGCAATGGCGCTGCTGATCACCANCCATTTCTCCCAACNTCTTCCNT 740  
Db 1 TCCACATGGCAATGGCGCTGCTGATCACCATTC-AGTACATCACCANCCGTCATCATTCAT 59  
QY 741 NGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 798  
Db 60 GGCTCTCCACATGCGACGCTGCAAGCCACCGGGAATGCCATGTGCTGCGACCTCTCTCT 119  
QY 799 ATGATG 806  
Db 120 CACTATGG 127

## RESULT 15

US-09-828-505-3  
; Sequence 3, Application US/09828505  
; Patent No. US20020142978A1  
; GENERAL INFORMATION:  
; APPLICANT: Raz, Eyal

APPLICANT: Takabayashi, Kenji  
APPLICANT: Nguyen, Minh-Duc  
TITLE OF INVENTION: Synergistic Improvements to  
FILE REFERENCE: 6510-203  
CURRENT APPLICATION NUMBER: US/09/828,505  
CURRENT FILING DATE: 2001-04-06  
PRIOR APPLICATION NUMBER: 60/195,890  
PRIOR FILING DATE: 2000-04-07  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 3  
LENGTH: 1137  
TYPE: DNA

ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: hsshadelta36ambal nucleic acid sequence

US-09-828-505-3

Query Match	5.18;	Score 41;	DB 10;	Length 1137;
Best Local Similarity	56.58;	Pred NO	0.0068;	

Matches 74; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

365 CGTGGGTTCAAGCAACCCGATCGACGACTGCTGGCGGTGCGACCCCTGATTGSCATGTCA 424

365 CGTGGGTTCAAGCAACCCGATCGACGACTGCTGGCGGTGCGACCCGTGATTGGCATGTCA 424

Db 74 CCTCCGAGCTTACACATTTATGATGGCTGTGGAGGGGGAAGCCAGATTGGGCCGAA 133

425 ACAGAAAAAGCTGCTGACTGCGGCATTGGCTTTGGACGCAACGCNATANGTGGCCGCG 484

Db 134 ACCGCAAGCAGTGGCTGACTGTGCCAAGTTTGGCAAGGTACGTCGGTGGCAAG 193

QY 485 ACGGGGAA TTT 495

Db 194 ACGGAGACATT 204

Search completed: June 19, 2003, 13:34:04  
Job time : 124 secs

Job time : 124 secs

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